

DR HSP; P02699; 1f88.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECPT_FL2; 1.
KW Receptor.
SQ SEQUENCE 447 AA; 48418 MW; E3DAAE5EE1F0FB99 CRC64;

Query Match 9.98; Score 217; DB 4; Length 447;
Best Local Similarity 22.58; Pred. No. 6.6e-11;
Matches 89; Conservative 65; Mismatches 130; Indels 112; Gaps 16;

QY 36 YPLSFQVSLTGFLMLEIVLGLGSLTIVLVLCMKSNLINSNIITMNLHVLDVIICVC 95
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 61 YAVIFLMVGNGMLIIIVVL-----SRRLVTYNFLLSLAYSDLLLAVAC 107

QY 96 IPLRIVILLSENLALICCFHEACVSF-----ASVSTAINVFATILDRYDISVKP--A 148
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 108 MPFTLLPLMGTFITFGTVIC----KAVSYLMGVSVSVST-LSLVAIALERYSAICRPLOA 162

QY 149 NRILTMGRAVMILSIIWFSSFLIPFIENVFS-----LOSNTWENKTILCVSTNE 202
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 163 RWTGRSHAARVIVATLLLSGL-LWPVPVYVVQPVGPRVLQCVRMP----- 211

QY 203 YYTELGMYYHLHVIQIPFFVFWVVMLITYTKILOALNIRIGTRF----- 246
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 212 --ANRVQTWSVLLLLLLFFIPGVMAVAGLISREL--YLGLREDGSDSDQSQRVNOG 267

QY 247 -----STGQKK-----ARKKKTISLTQHEDATMSQGSGGNVVF 283
|| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 268 GLPGAVHQNGRCRPETGAVGKDSGCYQLPRSRPALELA---LTAPGPGSGR----- 319

QY 284 VRTSVSVIALLRAVKRRERREKQKRFNRSLLIISFLFCWTPISVLNTILCLGPS- 342
| : : || : : || : : || : : || : : || : : || : : || : : || : : || : : ||
DB 320 -PTQAKLL-----AKKRVRMLLIVVLFCLVLPVYSANTWRAFDPGGA 363

QY 343 -DLVLKLRLCEL-VMAXGTTFTHPLLVAFTROKFKOK 376
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 364 HRALSGAPIFIIHLLSVASACVNPVLCFMHRFRQ 399

RESULT 14
Q98843 Q98843 PRELIMINARY; PRT; 458 AA.

AC Q98843
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DI 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dopamine D1B receptor.
GN D1B.
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7936;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97160583; PubMed=9006917;
RA Cardinaud B., Sugamori K.S., Coudouel S., Vincent J.D., Niznik H.B.,
RA Verdin P.;
RT "Early emergence of three dopamine D1 receptor subtypes in
RT vertebrates: Molecular phylogenetic, pharmacological, and functional
RT criteria defining D1A, D1B, and D1C receptors in European eel Anguilla
RT anguilla.";
RL J. Biol. Chem. 272:2778-2787(1997).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U62920; AAC60070.1; -;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL1; 1.

DR HSSP: P29274; 1MMH
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 422 AA; 46154 MW; 012335E0403F1890 CRC64;

Query Match 10.1%; Score 221; DB 6; Length 422;
Best Local Similarity 21.9%; Pred. No. 2.8e-11;
Matches 91; Conservative 69; Mismatches 153; Indels 102; Gaps 15;

QY 39 SFQV---SLTGFLMLEIVLGLGSLNLTVLVLYCKMSNLINSVSNITMNLHVLVDVLCVGC 95
DB 34 SYQVITSLGLTFLICAVLG---NACVVAIAIALERSLQN-VANYLIGSLAVTDLMSVLY 89

QY 96 IPLTIVILLSLSENALICCFHEACVSFASVSTAINVFAITLDRYDISVKPANRI--LT 153
DB 90 LPMAALVQVLNKNWTLGQVTCDFALDVLCTSSILHLCAIALDRYWAITDPIDYVKNRT 149

QY 154 MGRAVLMISIWIFSFPLPIEIVNFVLSQSGNTWENT--LLCVSTNEY---YTEL 207
DB 150 PRRAAALISLTIGLFLISIPPLM-----GWRTPEDRSDDPACTISKDHGVITYSTF 201

QY 208 GMYHLLVQIPIFFFTVVVVMILYTKILOALNIRIGTRFSTGOKKARKKTKISLTQHE 267
DB 202 GAFY-----IPL-----LLMLVLYGRIFRAARFRI-----RKTVKVKEKTGADTRHG 243

QY 268 ATDMSQ-----SSGRNVVFGVTSVSVIIALLRAVAK----- 299
DB 244 ASPAPQPKSVNGESGRNRLGVESKAGCALCANGAVROGDDGALEVIEVHRVGNKE 303

QY 300 -----RHRERRERQKRVFMSL-----LIISTFLLCWTPI 329
DB 304 HLPSPSEAGTPCAPASFERKERNAEAKR--KMLARERKTKVTLGLIIMGTFILCWLPF 361

QY 330 SVLNTTII-LCLGFSDLLVLRCLFLVMAYGTTIFHPLLYAFTQKQKVLKSKMK 383
DB 362 FIVALVLPFCSSCHMPTLLGAIINMLGYSNLLNPVIAFYFNKDFQNAFKKIIR 416

RESULT 11
Q92492
ID Q92492 PRELIMINARY; PRT; 396 AA.
AC Q92492;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cholecystokinin-B receptor/gastrin receptor (CCR-B gastrin receptor
DE Isoform) (Fragment).
GN CCKBR OR CCK-B.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=93352657; PubMed=8349705;
RA Ito M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima N.,
RA Nakata H., Chiba T., Chihara K.;
RT "Functional characterization of a human brain cholecystokinin-B
RT receptor. A trophic effect of cholecystokinin and gastrin.";
RL J. Biol. Chem. 268:18300-18305(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=94038108; PubMed=8222757;
RA Zimonjic D.B., Popescu N.C., Matsui T., Ito M., Chihara K.;
RT "Localization of the human cholecystokinin-B/gastrin receptor gene
RT (CCKBR) to chromosome 11p15.5-->p15.4 by fluorescence in situ
RT hybridization.";

RL Cytogenet. Cell Genet. 65:184-185(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=95151633; PubMed=7848914;
RA Ito M., Iwata N., Taniguchi T., Murayama T., Chihara K., Matsui T.;
RT "Functional characterization of two cholecystokinin-B/gastrin receptor
RT isoforms: a preferential splice donor site in the human receptor
RT gene.";
RL Cell Growth Differ. 5:1127-1135(1994).
RN [4]
RP SEQUENCE OF 16-26 FROM N.A.
RX MEDLINE=95194412; PubMed=7887934;
RA Miyake A.;
RT "A truncated isoform of human CCK-B/gastrin receptor generated by
RT alternative usage of a novel exon.";
RL Biochem. Biophys. Res. Commun. 208:230-237(1995).
DR EMBL; D21219; BAA04759.1; -;
DR EMBL; S76072; AAB33740.1; -;
DR HSSP; P02699; 1F88.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL2; 1.
FT NON_TER 396
SQ SEQUENCE 396 AA; 43252 MW; A25DD597CA903C0 CRC64;

Query Match 9.9%; Score 218; DB 4; Length 396;
Best Local Similarity 22.8%; Pred. No. 4.8e-11;
Matches 88; Conservative 70; Mismatches 136; Indels 92; Gaps 15;

QY 36 YPLSFQVSLRGFLMLEIVLGLGSLNLTVLVLYCKMSNLINSVSNITMNLHVLVDVLCVGC 95
DB 10 YAVIFLMSVGGNMLIIVVLGL-----SRRLRTVTNAFLSLAVSDLLAVAC 56

QY 96 IPLTIVILLSLSENALICCFHEACVSP-----ASVSTAINVFAITLDRYDISVKP--A 148
DB 57 MPFTLLPNLMTGTFIFGVIC-----KAVSYLMGVSVSVST--LSLVAIALERYSAICRPLQA 111

QY 149 NRILTGRAVLMISIWIFSFPLPIEIVNFSS-----LQSGNTWENTLVCVSTNE 202
DB 112 RVQWTRSHAARVIVATWLLSGL-LMWFPYVTVVQVPGVPRVLCQVHRPS----- 160

QY 203 YYTELGMYHLLVQIPIFFFTVVVVMILYTKILOALNIRIGTRF-----STGQKKARKK 257
DB 161 --ARVROTWSVLLLLLFIFPGVMAVAYGLISREL--YLGRLFDGSDSDSQRVNRQ 216

QY 258 KTLISLTQH-----EATDMSQSSGGRNVF-----GVRTSVSVIIA 293
DB 217 GLPGAVHQRCRPGTGAUGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLA 276

QY 294 LRAVKKHRRERQKRVFRMSLLIISTFLLCWTPIPSVLTILCLGPS--DLIVLKRLC 351
DB 277 -----KKRVVRLMLVIVVFLFCWLPVYSANTWRAFDGFGAHRALSGAPIS 322

QY 352 FL-VMAYGTTIFHPLLYAFTQKQK 376
DB 323 FIHLLSYASACVNPVYCFEMHRRFRQ 348

RESULT 12
Q9N296
ID Q9N296 PRELIMINARY; PRT; 422 AA.
AC Q9N296;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Serotonin receptor 1A.
GN HTR1A.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.


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Q23305
ID Q23305 PRELIMINARY; PRT; 539 AA.
AC Q23305;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 2C412.1 protein.
GN 2C412.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Ainscough R.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; 278067; CAB01528.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
SQ SEQUENCE 539 AA; 62655 MW; F2E750CCC7FE5C2D CRC64;

Query Match 10.2%; Score 224; DB 5; Length 539;
Best Local Similarity 21.2%; Pred. No. 2e-11;
Matches 89; Conservative 82; Mismatches 150; Indels 98; Gaps 14;

QY 25 DINTNMQPLSYPLSFQVSLTGFLMLE---IVLGLASNTLVLYCMKSLNSVSNIT 81
DB 11 DVNAILQPNQNDVLFPEVRL-GYSVLYFLTLIIGLVGGLITSILMKKL--SVANIFL 67
QY 82 MNHLVDVIVCGCIPLTIVILLLESNTALICCFHEACVSFASVSTAINVFAITLDY 141
DB 68 INLAVDLLCITAVPTTPVLAFLMKWIFGIIMCKLVPTCOAFSVLISWSLCYIAIDRY 127
QY 142 DISVKPANRLITMGRAVLMISWIFSFELPIEFVNFESLQSGNTWENKTL---LC- 197
DB 128 RSVTPLPREPWSDRHAWLMTFWVAFVLAFLYISQNLKTM-----VIENVLGDFCG 183
QY 198 -----VSTNEYTELGHYHLVQIPIFFFTVVVMVITYTKILOALNIRIGTRFSTG 249
DB 184 EFNQSDSEISKLYTTSL-----LIQLII---PAIMSFYLMILQKVQ----- 225
QY 250 QKKARKKKTISLTTOHEATDMSQSGGRNVFGRVTSVVIALLRRAVKRHRERQK 309
DB 226 -----TDWLVDG-----SMLTAAQQA-----QTAVRKR 249
QY 310 RVFRMSLLIISTFLCWTPLSVLN-----TTILCGPSDLLVKRLCLFLVMA 356
DB 250 RVMTVLIVVFMACQVFLVAFVLAFLYISQNLKTM-----VIENVLGDFCG 308
QY 357 YGTFIFHPLLYAFTRQKQVLSKSM-----KKRVSVIVEADPLPNNAVIHNSWID 407
DB 309 MTSIVNVPVLYFWMKSHRRALKDDMTWLTNARRHNVGLSRFTSPSPSVVYRRTLE 367

RESULT 7
Q9N298
ID Q9N298 PRELIMINARY; PRT; 422 AA.
AC Q9N298;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Serotonin receptor 1A.
GN HTR1A.

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OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHIMP-220;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB041404; BAA94489.1;
DR HSP; P29274; 1MMH;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 422 AA; 46171 MW; FCD989BD0313A1A0 CRC64;

Query Match 10.2%; Score 223; DB 6; Length 422;
Best Local Similarity 21.8%; Pred. No. 1.8e-11;
Matches 93; Conservative 73; Mismatches 157; Indels 104; Gaps 16;

QY 27 NTNNMQPLSYPLSFQV---SLTQFLMLEIVLGLSNTLVLYCMKSLNSVSNITNM 83
DB 24 NTSGISDVF--SYQVITSLLLGLTIFCAVLG---NACVVAALIALSLQN-VANYLIGS 77
QY 84 LHVLDVIVCGCIPLTIVILLLESNTALICCFHEACVSFASVSTAINVFAITLDYDI 143
DB 78 LAVTDLMSVSLVLPMAALYQVLNKNLTGLQVTCDFIALDVLCTSSLHLCAIALDRIYA 137
QY 144 SVKPANRI--LTMGRAVLMISWIFSFELPIEFVNFESLQSGNTWENKTL---LLCVS 199
DB 138 ITDPIDVYVNRTPRAAALSLTLWGLFSLIPML-----GWTPEDRSDPDACTI 189
QY 200 TNEY-----YTELGMVYHLVQIPIFFFTVVVMVITYTKILOALNIRIGTRFSTGQKKAR 255
DB 190 SKDHGYTIYTFGAFY-----IPL-----LLMLVLYGRIFRAARFRI-----RKTVK 231
QY 256 KKTISLTTOHEATDMSQ-----SSGRNVFGRVTSVVIALLRRAVK----- 299
DB 232 KVETGADTRHGASPAQPKKSVNGESGRNWRGLGSKAGGALCANGAVRQSGDDGALE 291
QY 300 -----RHREREROKRVFRMSL-----L 317
DB 292 VIEVHRVGNSEKHLPLPSEAGTPCAPASFERNKERNAEAKR--KMLAREKTVKTLGI 349
QY 318 IISTFLCWTPLSVLNTTI-LCLGPSDLLVKRLCLFLVMAVYGTTFIFHPLLYAFTRQKQK 376
DB 350 IMGTFILCWLFPFIFVALVLPFCSSCHMPTLLGAIINWLGYNSLLNPVIYAYENKDFON 409
QY 377 VLKSKMK 383
DB 410 AFKKIIR 416

RESULT 8
Q73734
ID Q73734 PRELIMINARY; PRT; 373 AA.
AC Q73734;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Neuropeptide Y/peptide YY receptor Yc.
GN NPYRVC OR NPYRVC.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

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Qy	96	IPLTIVILLLSLENTALICCFHEACVSP-----ASVSTAINFAITLDRYDISVKP--A	14
Db	108	MPETLLENMGTFIFGTVIC-----KAVSLMGVSVSVST-LNLVAIALERYSAICRPLQA	162
Qy	149	NRILTMGRAVMLMISWISFSEFLPIEFIEVFFS-----LQSGNTWENKTLCCVSTNE	202
Db	163	RVNQTRSHAARVILAWLLSLGL-LMVPYVYVYVQVGPVLIQCWHRWPS-----	211
Qy	203	YYTELGMYHLLVQIPIFFFTVVVMLITYTKILQALNIRIGTRF--STGQKKKARKKKTI	260
Db	212	--ARVROTWSVLLMLLFFPIPGVMAVAGLISREL--YGLRFEGDNDSDTQFSVRNOG	267
Qy	261	SLTQHEATDMSSOSSGRNVVFCVTSVIAIALRA-----VKRHRER	304
Db	268	GLPGTAGPVGPHVGGCRHVTVAGEDNDGCVQLPRSLRMTLLTPTPGPGGLASANOAK	327
Qy	305	REQKRVFRMSLLIISTFELCWPTISVLNNTTILCLGPS--DLLVKLRCLFL-VMAYGTTI	361
Db	328	LLAKRVVRMLLVILLFFELCWLPITYSANTWRAFDGGAHRALSGAPISFIHLLSYASAC	387
Qy	362	FHPLLYAFTQKFEK 376	
Db	388	VNPLVYCFMHRFRQ 402	
RESULT 4			
O57463			
AC	ID	O57463 PRELIMINARY; PRT; 375 AA.	
AD	O57463;		
DT	01-JUN-1998 (T-EMBLrel. 06, Created)		
DT	01-JUN-1998 (T-EMBLrel. 06, Last sequence update)		
DT	01-DEC-2001 (T-EMBLrel. 19, Last annotation update)		
DE	Neuropeptide Y /peptide YY receptor Yb.		
DN	NPYRYB.		
OS	Brachydanio rerio (Zebrafish) (Zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxId=7955;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RA	Lundell I., Berglund M.M., Starback P., Salaneck S., Gehlert D.R.,		
RA	Larhammar D.;		
RT	"Cloning and characterization of a novel neuropeptide Y (NPY) receptor		
RT	subtype in the zebrafish.";		
RL	DNA Cell Biol. 0:0-0(1997).;		
DR	EMBL; AF030245; AAB94616.1; -.		
DR	ZFIN; ZDB-GENE-980526-208; npyryb.		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHHODOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1.1; UNKNOWN_1.		
DR	PROSITE; PS50262; G_PROTEIN_RECP_F1.2; 1.		
KW	Receptor.		
SQ	SEQUENCE 375 AA; 42116 MW; 4B0C9551131A14D1 CRC64;		
Query Match 10.5%; Score 229.5; DB 13; Length 375;			
Best Local Similarity 21.5%; Pred. No. 4.4e-12;			
Matches 81; Conservative 76; Mismatches 114; Indels 105; Gaps			
Qy	42	VSLTGFLMLE-----IVLGLSGNITVLVLYCMKSNLINSVSNITNMLHVLVDIIVCGCIP	97
Db	22	LSSTFLIVAYSTMALVGLVGN-TCLVWVITROKEMRNVTNIFVNLSCDILVCLVCLIP	80
Qy	98	LTIVILL-----SLESNTALICCFHEACVSVASVAINVFA---ITLDRYDISVKP	147
Db	81	VTIITYTLMDRWILGEALCKVTPFVQC-----MSVTVSIFSMVLIALERHQLIHP	130
Qy	148	ANRLTMGRAVMLMISWISFSEFLPIEFIEVFFSILQSGNTWENKTL-----LCV	198
Db	131	TGWKPVVRHSTVLAIVWIIATCF-ISPUSF---FNLINSPHNLSLFPNPFSDHFIC	186
Qy	199	STNEYVELG--MYHLLVQIPIFFFTVVVMLITYTKILQALNIRIGTRFSGCKKARK	256

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Db 187 ---EQWSEGNRLTYTTLLQCYCLALILVCYPRIFRL-----SRR 316
Qy 257 KKTISLTQHEATDMSOSSGGRNVVFGVRTSVSIIALRRVKKHRREROKRVFMSL 316
Db 229 KDMV-----ERAGGR-----QKKAGSRVAVMLA 254
Qy 317 LIISTFLLCWTPISVLNTTI-----LCGPSDLLVKLRLCFLVMAYGTTTFHPLLXA 368
Db 255 SIVAAFAFALCWPLNVFNTIFDWNHEAPVC-QHDAL--FSACHLT-AMASTCVNPIYG 309
Qy 369 FTROKFOKVLKSKMKK 384
Db 310 FLNNNFQELKSLSR 325

RESULT 5
Q8QGM3 PRELIMINARY; PRT; 377 AA.
ID Q8QGM3
AC Q8QGM3;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Neuropeptide Y receptor 4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Atherosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundell I., Boswell T., Larhammar D.;
RT "Chicken Neuropeptide Y Family Receptor Y4; a Receptor with Equal
RT Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide YY."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410853; AAL84161.1; -.
KW Receptor.
SQ SEQUENCE 377 AA; 42972 MW; C9EGC6C0DBDFD1F9E CRC64;

Query Match 10.3%; Score 225; DB 13; Length 377;
Best Local Similarity 23.5%; Pred. No. 1.1e-11;
Matches 96; Conservative 74; Mismatches 131; Indels 108; Gaps

Qy 27 NTNNYQPLSY--LSFQ----VSLTGFL----MLEIVLGLGSNLTVLVLYCMKSNLSNV 76
Db 16 NKNLSSNRSPSHLSNQRNVDTLTVEFATSYSLTVLGIVGNICLAVIARQKKTN-V 74
Qy 77 SNIITMNLHVDVVICVCGPIPLTVILLLESNTALICCFHCAVSF----ASVSTAI-N 132
Db 75 TNLISLNLIIISDLFMCLVCLPFTVYVYTMDDYWIPEGYMC----KMTSFTQCTSVTVSILS 130
Qy 133 VFATLDRYDISVQPNRIITMGRVLMISITIFSFSLPIPIEVNFTFSLOGNTWEN 192
Db 131 LVLIALERHQILINPTGWRPSISQAYIGIVMTLACIMSL-PFLTP---SILSNDIYEQ 186
Qy 193 KT-----LLCVST--NEYYPELGMYYHLVQ--IRIFFFTVVVMLITYTKILQALN 239
Db 187 LSHIMNFSYDKAICIDSWPSEQHRLIYTTLLLLQYCIPLFF-----IILCYLRIYLR- 240
Qy 240 IRICTRFSTGQKKARKKKTISLTQHEATDMSOSSGGRNVVFGVRTSVSIIALRRVK 299
Db 241 -----QKKR-----DMFEKS----- 250
Qy 300 RHREREROKRVFMSLLI---ISTFLLCWTPISVLNTTI-----LCGPSDLLVKLRCLCF 352
Db 251 ---RYSNAGRLRINTILLASMAFAFVCMPLPHVFNTIVDWNKYKILSPCHHNLIFSLSCH 307
Qy 353 LVMAYGTTIFHPLIYAFTROKFOKVLKS-----KMKRVVSVIVEADPLP 396
Db 308 LV-AMASTCVNPIYGFNLNSFKKEVKSLLISCOHNSVTASIEDYDHLPL 355

RESULT 6

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RESULT 6

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Db 116 TTTTFFGTSVSVSTNLVAISLERYGCAICRPLQSRVWTKSHALKVIAATWCLSTIMTP 175
QY 170 ---FSLFIPFIEVN-----FFSLQSG---NTWENKTLVCVSTNEYTELGMYYHLLVQ 216
Db 176 YPIYSLNLPVFTKNNQNTANMCRFLLPSDAMQOSWQTFLLI----- 216
QY 217 IPIFFTVVVMILITVKILQALNIRIGTRFSTGQKKARKKTKTI-----SLTQHEA 268
Db 217 --LFLIPGVWVAYGLI--SLELYQGIKFDASQKSAKRLSSGGGGSSSSRYED 272
QY 269 TD-----MSQSSGGGRNVFVGVTSVSV--IIALRAVKKHRRRRRQ 308
Db 273 SDGCVLQSRPRKLEQLQSTSSSGR--INRIRSSGAANLIA-----K 316
QY 309 KRVRMSLLIISTFLCWTPTISVLNT-----TI-----LCLGPSDLLVKRLCFLVMAYG 358
Db 317 KRVRMLIVIVVFLCWPMPFISANAWRAYDTVSAEKHLSTGTPISFI-----LLLSYT 369
QY 359 TTIFHPLLYAFTROKFQ 375
Db 370 SSCVNPIIYCFMKNKRFR 386

RESULT 2
Q9DBV6 PRELIMINARY; PRT; 436 AA.
AC Q9DBV6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200012013, full insert sequence.
GN CCKAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004730; BAB23512.1; -.
DR HSSP; P02699; IF88.
DR MGD; MGI:99478; Cckar.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01570; NFFRRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 436 AA; 48446 MW; 49B4AD57F080F08A CRC64;
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Query Match 12.1%; Score 266; DB 11; Length 436;
Best Local Similarity 23.8%; Pred. No. 3.2e-15;
Matches 104; Conservative 85; Mismatches 128; Indels 120; Gaps 20;

QY 6 ILEINMQSESNTIVRDDIDDINTNMV---QP---LSYPLSFQVSLTGFLMLRIVLGLGSN 59
Db 3 VVDSLLANGSNITPPCELGLENELFCLDQPHPSKEWQSAVOILLYSFIFLVSVLGDTLV 62
QY 60 LTVLVLYCMKSNLINSVNIITMNLHVLVDIICVGCIPLTIVILLLESNTALICCFFE 119
Db 63 ITVLI---RNKMRVTNIFLLSLAVSDMLCLFCMPFNLPNLLKDFIFGSVC---K 115
QY 120 ACVSFASVSTAINVF---AITLDRYDISVKP-ANRI-LTMGRAVMLMISINIFSP----- 169
Db 116 TTTTFFGTSVSVSTNLVAISLERYGCAICRPLQSRVWTKSHALKVIAATWCLSTIMTP 175
QY 170 ---FSLFIPFIEVN-----FFSLQSG---NTWENKTLVCVSTNEYTELGMYYHLLVQ 216
Db 176 YPIYSLNLPVFTKNNQNTANMCRFLLPSDAMQOSWQTFLLI----- 216
QY 217 IPIFFTVVVMILITVKILQALNIRIGTRFSTGQKKARKKTKTI-----SLTQHEA 268
Db 217 --LFLIPGVWVAYGLI--SLELYQGIKFDASQKSAKRLSSGGGGSSSSRYED 272
QY 269 TD-----MSQSSGGGRNVFVGVTSVSV--IIALRAVKKHRRRRRQ 308
Db 273 SDGCVLQSRPRKLEQLQSTSSSGR--INRIRSSGAANLIA-----K 316
QY 309 KRVRMSLLIISTFLCWTPTISVLNT-----TI-----LCLGPSDLLVKRLCFLVMAYG 358
Db 317 KRVRMLIVIVVFLCWPMPFISANAWRAYDTVSAEKHLSTGTPISFI-----LLLSYT 369
QY 359 TTIFHPLLYAFTROKFQ 375
Db 370 SSCVNPIIYCFMKNKRFR 386

RESULT 3
P89005 PRELIMINARY; PRT; 450 AA.
AC P89005;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gastrin/cholecystokinin-B receptor (fragment).
DE Prآموس natalensis (African soft-furred rat) (Mastomys natalensis).
DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
DE Mastomys
OX NCBI_TaxID=10112;
RN [1]
RP SEQUENCE FROM N.A.
RL Luque E.A., Tang L.H., Modlin I.M.;
RT "Gastrin receptor expression in Mastomys natalensis.";
RT Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49834; AAB41677.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 450 AA; 48792 MW; 333F4C368B7A0A97 CRC64;

Query Match 10.7%; Score 235.5; DB 11; Length 450;
Best Local Similarity 23.5%; Pred. No. 1.6e-12;
Matches 88; Conservative 71; Mismatches 149; Indels 67; Gaps 13;

QY 36 YPLSFQVSLTGFLMLRIVLGLGSNLTVLVYCMKSNLINSVNIITMNLHVLDIICVGC 95
Db 61 YAVIFLMSIGGNMLIIVLGL-----SRLRTVTNAPFLSLAVSLLAVAC 107
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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 15:59:53 ; Search time 35 Seconds
(without alignments)
2549.097 Million cell updates/sec

Title: US-09-845-721-2
Perfect score: 2192
Sequence: 1 MCFSPLEINMQSESNITVR.....ITFDESEIRRLVPQVYTD 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	267	12.2	436	11	Q8VCC7	Q8vcc7 mus musculus
2	266	12.1	436	11	Q8BV6	Q8bvv6 mus musculus
3	235.5	10.7	450	11	P89005	P89005 pronomys nat
4	229.5	10.5	375	13	O57463	O57463 brachydanio
5	225	10.3	377	13	Q8QGM3	Q8qgm3 gallus gall
6	224	10.2	539	5	Q23305	Q23305 caenorhabdi
7	223	10.2	422	6	Q9N298	Q9n298 pan troglod
8	222	10.1	373	13	Q73734	Q73734 brachydanio
9	222	10.1	643	5	O62059	O62059 caenorhabdi
10	221	10.1	422	6	Q9N297	Q9n297 gorilla gor
11	218	9.9	396	4	Q92492	Q92492 homo sapien
12	217	9.9	422	6	Q9N296	Q9n296 pongo pygma
13	217	9.9	447	4	Q16144	Q16144 homo sapien
14	217	9.9	458	13	Q98843	Q98843 anguilla an
15	216	9.9	399	5	Q9NG02	Q9ng02 apis mellif
16	215.5	9.8	518	6	Q9MY18	Q9my18 oryctolagus

17	213.5	9.7	464	5	O9G054	O9g054 aedes aegyp
18	213	9.7	396	4	O75824	O75824 homo sapien
19	211.5	9.6	390	6	Q8WNV9	Q8wnv9 sus scrofa
20	211.5	9.6	440	5	Q9N324	Q9n324 caenorhabdi
21	211	9.6	377	5	O02464	O02464 manduca sex
22	209.5	9.6	365	13	Q8UVW7	Q8uvw7 lampetra fl
23	209	9.5	515	11	O9DBL0	O9db10 mus musculu
24	208.5	9.5	516	4	Q9NYK7	Q9nyk7 homo sapien
25	208	9.5	379	5	O76124	O76124 papilio xut
26	206	9.4	380	5	Q9UAM7	Q9uam7 papilio gla
27	205.5	9.4	374	13	Q9VHX1	Q9vhl1 gadus morhu
28	205.5	9.4	402	5	Q964E5	Q964e5 dugesia tig
29	205.5	9.4	516	4	Q96LC6	Q96lc6 homo sapien
30	205	9.4	408	13	Q98998	Q98998 xenopus lae
31	204	9.3	383	6	Q9GK75	Q9gk75 macaca mula
32	203	9.3	487	6	Q9N2B1	Q9n2b1 gorilla gor
33	201.5	9.2	310	13	Q8QGK6	Q8qgx6 fuqu rubrip
34	201.5	9.2	446	6	Q8WND7	Q8wnd7 bos taurus
35	201	9.2	474	11	Q8R456	Q8r456 ratus norv
36	200	9.1	377	13	O73733	O73733 brachydanio
37	200	9.1	477	5	Q9BMA9	Q9bma9 mamestra br
38	199	9.1	419	5	O77254	O77254 boophilus m
39	199	9.1	457	5	Q18534	Q18534 caenorhabdi
40	197.5	9.0	390	4	Q96LD9	Q96ld9 homo sapien
41	197	9.0	372	13	P79945	P79945 xenopus lae
42	197	9.0	471	13	Q8UUG8	Q8uug8 tetraodon f
43	197	9.0	487	6	Q9N2B2	Q9n2b2 pan troglod
44	196	8.9	381	5	Q95YI3	Q95y13 bombyx mori
45	196	8.9	660	5	Q9VFW5	Q9vfw5 drosophila

ALIGNMENTS

RESULT 1

Q8VCC7	Q8VCC7	PRELIMINARY;	PRT;	436 AA.
AC	Q8VCC7;			
DT	01-MAR-2002 (TReMBLrel. 20, Created)			
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)			
DE	Cholecystokinin A receptor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=KIDNEY;			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC020534; AAH20534.1; -			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm1.1; 1.			
DR	PRINTS; PRO0237; GPCR_RHODOPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1.1; UNKNOWN_1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1.2; 1.			
KW	Receptor.			
SQ	SEQUENCE 436 AA; 48396 MW; FD35D8453B792F79 CRC64;			

Query Match 12.2%; Score 267; DB 11; Length 436;
Best Local Similarity 23.8%; Pred. No. 2.6e-15;
Matches 104; Conservative 85; Mismatches 128; Indels 120; Gaps 20;

Qy	6	ILEINMQSESNITVRDIDDINTNMV-----QP-LSYPLSFQVSLTGLMLEIVLGLGSN	59
Db	3	VVDSLLMNGSNITPPCELGLENFTLFCDDQPQSKENQSAVQILLYSFIFLSVLGNFLV	62
Qy	60	LTVLVLCMKSNLINSVNIITMNLHVLDTVICVGCPLTIVILLLSLESNTALICFHE	119
Db	63	ITVLV-----RNKRMRVTNIFLLSLAVSDMLCLFCFPNLPNLKDFIGSAVC---K	115
Qy	120	ACVSFASVSTAINVF---ATLDRYDISVKP-ANRI-LTMGRVLMISIWFSF-----	169

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FT TRANSMEM 132 150 3 (POTENTIAL).
FT DOMAIN 151 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 189 4 (POTENTIAL).
FT DOMAIN 190 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 242 5 (POTENTIAL).
FT DOMAIN 243 333 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 334 355 6 (POTENTIAL).
FT DOMAIN 356 373 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 374 394 7 (POTENTIAL).
FT DOMAIN 395 447 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 127 205 BY SIMILARITY.
FT LIPID 408 408 PALMITATE (BY SIMILARITY).
FT CONFLICT 171 171 A -> P (IN REF. 5).
FT CONFLICT 249 249 L -> V (IN REF. 5).
SQ SEQUENCE 447 AA; 48419 MW; BAEFAD4C1F85915 CRC64;
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Query Match 9.9%; Score 218; DB 1; Length 447;
Best Local Similarity 22.8%; Pred. No. 6.1e-08;
Matches 88; Conservative 70; Mismatches 136; Indels 92; Gaps 15;

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QY 36 YPLSFQVSLTGFLMLREIVLGLSGNLVFLVLYCMKSLNSVSNITMNLHLVLDVVICVGC 95
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 YAVIFLMSVGGNMLIIVLGL-----SRRLRTVTVNAFLLSLAVSDELLAVAC 107

QY 96 IPTIVILLLSLESTALICCFHEACVSF-----ASVSTAINVFAITLDRYDISVRP--A 148
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 108 MPFTLLPNLMGTIFGTVIC---KAVSYLMGVSVSVST-LSLVAIALERYSAICRPLQA 162

QY 149 NRLLTWGRAVMLMISTWIFSPFLPFIEVNFPS-----IQSGNTWENKTLICVSTNE 202
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 163 RVWQTRSHAARVIVATLLSGL-LMVPYPVYTVVQVGPVQLQCVHRWPS----- 211

QY 203 YYTELGMVYHLLVQIPFEFTVVVMLITYTKILQALNIRIGTRF-----STGQKKKARKK 257
   : : : : : : : : : | : | : | : | : | : | : | : | : | : | : |
Db 212 --ARVQRTWSVLLLLLFIPGVVMAVAYGLISREL--YLGRLFDGSDSDSOSRVRNQ 267

QY 258 KTISLATQH-----EATDMSQSSGGRNVVF-----GVRTSVSVIIA 293
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 268 GLPGAVHQNCRCRPEYCAVGEDSDGCVQLPRSRPALELTALTAPGPGSRPTQAKLLA 327

QY 294 LRAVKRHRERRQRKRVFMSLLIISTELLWCWTPISVNLTTILCLGPS--DLLVKRLC 351
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 328 -----KKRVVRLLVIVVLFELCWLPVYSANTWRAFDGPGAHRLSGAPIS 373

QY 352 FL-VMAYGTIFHPHLLYAFTRQFQK 376
   | : : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 374 FIHLLSYACVNPLVYCFMHRFRQ 399
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Search completed: December 4, 2002, 16:01:36

Job time : 15 secs

FT	DOMAIN	1	52	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	53	75	1 (POTENTIAL).
FT	DOMAIN	76	90	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	91	111	2 (POTENTIAL).
FT	DOMAIN	112	128	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	129	150	3 (POTENTIAL).
FT	DOMAIN	151	171	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	172	194	4 (POTENTIAL).
FT	DOMAIN	195	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	212	232	5 (POTENTIAL).
FT	DOMAIN	233	295	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	296	316	6 (POTENTIAL).
FT	DOMAIN	317	333	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	334	354	7 (POTENTIAL).
FT	DOMAIN	355	370	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	5	5	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	127	205	BY SIMILARITY.
SO	SEQUENCE	370 AA;	41201 MW;	0553C62B12DAAD84 CRC64;
Query Match 10.08; Score 218.5; DB 1; Length 370;				
Best Local Similarity 23.48; Pred. No. 4.7e-08;				
Matches 89; Conservative 56; Mismatches 141; Indels 95; Gaps 12;				
Qy	39	SFOVSLTGFLMLEIVGLGSLNLTVLVLYCKMKSNLINSVSIITMNLRLVDLVIICGCIPL	98	
Db	50	AFTVLVTVLLVLLAATFLWNLVLVT-ILRVAFHRVPHNLVASTAVSDVLVAVLWPL	108	
Qy	99	TIVILL-----LSLENTALICCFHEACVSFASVSTAINVFAITLDRY-	141	
Db	109	SLVSELSAGRWRQLGRSLCHVWISFD-----VLCC-----TASINWVAIALDRYW	154	
Qy	142	DISVKPANRILTMGRAYVLMISI-WISFFSFLPIFFIEVNFSSQSGNTWENKILLCVST	200	
Db	155	TITRHLQYTLTTRSRALMTAITWALSIALAPLL-----FGWGEAYDARLQRCQVS	208	
Qy	201	NEYVTELGMVYHLLVQIPFPFTVVMVLTITKILQALNIRIGTF-----STGQKKK	253	
Db	209	QE-----PSVAVSTCGAFPLVAVLVFYWKYKAKFFGRRRAVPLPATYTAKE	262	
Qy	254	ARKKKTSLTQHEATDMSQSSGGRNVFVRTSVVIALRAVKRHRERRRQKRVFR	313	
Db	263	APPESENVFTARRATVTFQTSG-----DSWREQEKRAAM	298	
Qy	314	MSLLIITFLCWTPISVLNTITILCLGPSDLLVLRLC-----FLWYAGTTTFHP	364	
Db	299	MVGLIGVFLWCWIPFL-----TELISPLCACSLPPIWKSIFLWLGYSNSFPNP	348	
Qy	365	LLYAFTRQKFQKVLKSKMKR	385	
Db	349	LIYAFKNKNYNAEKSLETKQ	369	
RESULT 15				
OC	GASR_HUMAN	STANDARD;	PRT;	447 AA.
AC	P32239;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR).			
GN	CCKBR OR CCKRB			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=93216795; PubMed=7681836;			
RA	Lee Y.-M., Beinborn M., McBride E.W., Lu M., Kolakowski L.F. Jr.,			
RA	Kopin A.S.;			
RT	"The human brain cholecystokinin-B/gastrin receptor. Cloning and			
RT	characterization."			

RL	J. Biol. Chem. 268:8164-8169(1993).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=93080572; PubMed=1280419;
RA	Pisegna J.R., de Weerth A., Huppi K., Wank S.A.;
RT	"Molecular cloning of the human brain and gastric cholecystokinin
RT	receptor: structure, functional expression and chromosomal
RT	localization."
RL	Biochem. Biophys. Res. Commun. 189:296-303(1992).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Placenta;
RX	MEDLINE=94022320; PubMed=8415658;
RA	Song I., Brown D.R., Wiltshire R.N., Gantz I., Trent J.M.,
RA	Yamada T.;
RT	"The human gastrin/cholecystokinin type B receptor gene: alternative
RT	splice donor site in exon 4 generates two variant mRNAs.";
RL	Proc. Natl. Acad. Sci. U.S.A. 90:9085-9089(1993).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=93352657; PubMed=8349705;
RA	Ito M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima N.,
RA	Nakata H., Chiba T., Chihara K.;
RT	"Functional characterization of a human brain cholecystokinin-B
RT	receptor. A trophic effect of cholecystokinin and gastrin.";
RL	J. Biol. Chem. 268:18300-18305(1993).
RN	[5]
RP	SEQUENCE FROM N.A.
RC	TISSUE=temporal cortex;
RA	Tate S.N., Gray J., Denyer J., Stolz M., Foord S., Lee M.G.;
RA	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC	-1- FUNCTION: RECEPTOR FOR GASTRIN AND CHOLECYSTOKININ. THE CCK-B
CC	RECEPTORS OCCUR THROUGHOUT THE CENTRAL NERVOUS SYSTEM WHERE THEY
CC	MODULATE ANXIETY, ANALGESIA, AROUSAL, AND NEUROLEPTIC ACTIVITY.
CC	THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS
CC	THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC	SYSTEM.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; L08112; AAA35657.1; -
DR	EMBL; L04473; AAA35660.1; -
DR	EMBL; L10822; AAC37528.1; -
DR	EMBL; D13305; BAA02564.1; -
DR	EMBL; L07746; AAA91831.1; -
DR	PIR; JC1352; JC1352.
DR	PIR; A46645; A46645.
DR	PIR; A47430; A47430.
DR	HSP; P02699; 1F88.
DR	Genew; HGNC:1571; CCKBR.
DR	MM; 118445;
DR	Interpro; IPR000276; GPCR_Rhodpsn.
DR	Fram; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR	PROSITE; PS00262; G_PROTEIN_RECF_F2_1; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Lipoprotein; Palmitate.
FT	DOMAIN 1 57
FT	TRANSSEM 58 79
FT	DOMAIN 80 87
FT	TRANSSEM 88 109
FT	DOMAIN 110 131
FT	EXTRACELLULAR (POTENTIAL).
FT	1 (POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	2 (POTENTIAL).
FT	EXTRACELLULAR (POTENTIAL).

QY 36 YPLSFQVSLTGLFMLEIVLGLSGLNLTIVLYCMKSNLINSVNIITMNLHVLVDVICVGC 95
Db 61 YAVIFLMSGGNNLITVVLGL-----SRLRTVTNAFLLSLAVSDLLAVAC 107
QY 96 IPLTIIVILLLESNTALICCFHEACVSF-----ASVSTAINVFAITLDRIYDISVKP--A 148
Db 108 MPTLPLNLMGTFIFGTVIC-----KAVSYLMGVSVSVST-LNLVALALERYSAICRPLQA 162
QY 149 NRILTMGRAVLMMSIWISFESFPIEFVNFES-----LQSGNTWENKTLICVSTNE 202
Db 163 RVWQTSRSHAARVILATWLLSGL-LMVPYVYTVVQVGPVRLQCMHWFS----- 211
QY 203 YTELOMGYHLLVQIPIFFETVVVVMITTKILQALNIRIGTRF--STGQKKKARKKKT 260
Db 212 --ARVQTWSVLLMLLFFIPGVMAVAYGLISREL--YLGRLFDGDNDSQTSVRNQG 267
QY 261 SLTQHEATDMSQSGRNVFVGRTSVSVIILRA-----VKRHRER 304
Db 268 GLPGGTAPGPHONGCRHVTVVAGEDNOCGYVOLPKSRLEMTLTTPPTGPGGLASANOAK 327
QY 305 RERQKRVFRMSLLIISTFLLCWTPISVLNLTILCLGPS--DLLVKRLCLFL-VMAYGTTI 361
Db 328 LLAKKRVVRMVLVIVLFFELCMLPIYSANTWCAFDGPGAHRAISGAPISFIHLLSYASAC 387
QY 362 FPHLLYAFTRQFQK 376
Db 388 VNPLVYCFMHRFRQ 402
RESULT 11
GASR_MOUSE STANDARD; PRT; 453 AA.
AC P56481;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gastrin/cholecystokinin type B receptor (CKC-B receptor) (CKC-BR).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA KopIn A.S.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=20318371; PubMed=10860839;
RA Lay J.M., Jenkins C., Frlis-Hansen L., Samuelson L.C.;
RT "Structure and developmental expression of the mouse CKC-B receptor gene";
RL Biochem. Biophys. Res. Commun. 272:837-842(2000).
CC -!- FUNCTION: RECEPTOR FOR GASTRIN AND CHOLECYSTOKININ. THE CKC-B RECEPTORS OCCUR THROUGHOUT THE CENTRAL NERVOUS SYSTEM WHERE THEY MODULATE ANXIETY, ANALGESIA, AROUSAL, AND NEUROLEPTIC ACTIVITY. THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF019371; AAB71863.1; -;
DR EMBL; AF264178; AAG09801.1; -;

DR EMBL; AF264177; AAG09801.1; JOINED.
DR MGD; MGI:99479; Cckbr.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
Db 108 MPTLPLNLMGTFIFGTVIC-----KAVSYLMGVSVSVST-LNLVALALERYSAICRPLQA 162
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Lipoprotein; Palmitate.
FT DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 58 79 1 (POTENTIAL).
FT DOMAIN 80 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 150 3 (POTENTIAL).
FT DOMAIN 151 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 189 4 (POTENTIAL).
FT DOMAIN 190 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 242 5 (POTENTIAL).
FT DOMAIN 243 339 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 340 361 6 (POTENTIAL).
FT DOMAIN 362 379 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 380 400 7 (POTENTIAL).
FT DOMAIN 401 453 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 127 205 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 414 414 BY SIMILARITY.
FT PALMITATE (BY SIMILARITY).
SQ SEQUENCE 453 AA; 49171 MW; DFD21432C323405C CRC64;
Query Match 10.3%; Score 226; DB 1; Length 453;
Best Local Similarity 22.6%; Pred. No. 1.8e-08;
Matches 93; Conservative 78; Mismatches 159; Indels 82; Gaps 15;
QY 2 CESPILINMQSESNTVTRDDIDDTNNMYQPLSYPLSFQVSLTGLFMLEIVLGLSGLT 61
Db 39 CETPRIRGTGTRLELTIRTL-----YAVIFLMSVGGNVLITVVLGL----- 81
QY 62 VLVLYCMKSNLINSVNIITMNLHVLVDVICVGCIPLTIVILLLESNTALICCFHEAC 121
Db 82 -----SRLRTVTNAFLLSLAVSDLLAVACMPTLTPLNLMGTFIFGTVIC----KA 129
QY 122 VSF-----ASVSTAINVFAITLDRIYDISVKP--ANRILTMGRAVLMMSIWISFESFLI 174
Db 130 VSYLMGVSVSVST-LNLVALALERYSAICRPLQARVWQTSRSHAARVILATWLLSGL-LMW 187
QY 175 PTIEVNFES-----LQSGNTWENKTLICVSTNEYTELGMYHLLVQIPIFFETVVVVM 228
Db 188 PVPYTVVQVGPVRLQCMHWFS-----RVQMMSVLLILLFFIPGVVMA 235
QY 229 ITVTKILOALNIRIGTRF--STGQKKKARKKKTISLTQHEATDMSQSGRNVFVG-- 284
Db 236 VAYGLISREL--YLGRLFDGDNDSQTSVRNOCGLPGGAAAPGPHONGGCRHVTSLTG 293
QY 285 RTSVSVIILRA-----VKRHRERERQKRVFRMSLLIISTFLLCWT 327
Db 294 EDSGCVVQLPRSRLEMTLTTPPTGPGPRPNQAKLLAKRVRMVLVIVLFFVCWL 353
QY 328 PLSVNTTILCLGPS--DLLVKRLCLFL-VMAYGTTIFPHPLLYAFTRQFQK 376
Db 354 PVSANTWRAFDGPGARRALAGAPISFIHLLSYTSACANPLVYCFMHRFRQ 405
RESULT 12
GASR_RAT
ID GASR_RAT STANDARD; PRT; 452 AA.
AC P30553;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Gastrin/cholecystokinin type B receptor (CKC-B receptor) (CKC-BR).
GN CCKBR.

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DR EMBL; D86521; BAA13104.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 69 1 (POTENTIAL).
FT TRANSMEM 70 90 2 (POTENTIAL).
FT DOMAIN 91 110 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 111 132 3 (POTENTIAL).
FT DOMAIN 133 152 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 153 174 4 (POTENTIAL).
FT DOMAIN 175 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 230 5 (POTENTIAL).
FT DOMAIN 231 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 284 6 (POTENTIAL).
FT DOMAIN 285 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 321 7 (POTENTIAL).
FT DOMAIN 322 371 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 109 196 BY SIMILARITY.
FT LIPID 336 336 PALMITATE (POTENTIAL).
SQ SEQUENCE 371 AA; 42447 MW; 5847E358E320F24 CRC64;

Query Match 10.8%; Score 237.5; DB 1; Length 371;
Best Local Similarity 23.0%; Pred. No. 2.5e-09;
Matches 87; Conservative 59; Mismatches 128; Indels 105; Gaps 15;
QY 52 IVLGSGSLTVLVLCMKSLNSVSIITMNLVLDVLCVGCPLTIVLLLS--LES 109
DB 46 LIMGICGNLSLTIIFKQREAGQNTNLIANLSDLVCVCPFFAIYTLMDRWIFG 105
QY 110 NTALCCPHEACVSPASVSTAI-NVFATLDRIYDSVSPANKRLTMGRVLMISIWIFS 168
DB 106 NT---MCKLTSYQSVSISVFSVLVLAERYQLVNPGRGWKPSASHAYGIMLWLFS 162
QY 169 FFSFLIPFI-----EVNFFSLQSGNTWENKTLVCV-----STNE--YYTELGYHYHLV 215
DB 163 LL-LSLPILLSVHLDEPRNLSLPTDLYSHVVCVEMWPSKTNQLLYSTSLIMIQYP-- 219
QY 216 QIPIFFFTVVMILTYTKILQALNIRIGTRFSTGOKKARKKKTISLTQHEATDMSQSS 275
DB 220 -VPLGF-----MFICYLKVICLHR----- 239
QY 276 GGRNVVFGVTSVSVIIARRAVKRRRRER---OKRVFRMSLLIISTFLCWTPISVL 332
DB 240 -----NSKIDRRRENSRLTENKINTMLISIVTVFAACWPLNTE 280
QY 333 NT-----TILCLGSDLLVLRCLFLVAYGCTTFTHPLLAYFTQKQK----- 376
DB 281 NVIFDWMYHEVLMSCSHDLV--FAICHLV--AMVSTCINPLFYGLFNRNFQKDLVLIHCL 337
QY 377 --VLKSKMKRVVSVIAD 393
DB 338 CPALRERYENIAISLHTD 356

RESULT 10
GASR_PRNA

ID AC GASR_PRNA STANDARD; PRT; 450 AA.
DT P30796;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Gasrin/cholecystokinin type B receptor (CKK-B receptor) (CKK-BR).
GN CCKBR.
OS *Prionomys natalensis* (African soft-furred rat) (*Mastomys natalensis*).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OX NCBI_TaxID=10112;
RN [1]
RP SEQUENCE FROM N.A. PubMed=1530611;
RX MEDLINE=92412082; PubMed=1530611;
RA Nakata H., Matsui T., Ito M., Taniguchi T., Naribayashi Y., Arima N.,
RA Nakamura A., Kinoshita Y., Chihara K., Hosoda S., Chiba T.;
RT "Cloning and characterization of gastrin receptor from ECL carcinoma
tumor of *Mastomys natalensis*.";
RL Biochem. Biophys. Res. Commun. 187:1151-1157(1992).
CC -!- FUNCTION: RECEPTOR FOR GASTRIN AND CHOLECYSTOKININ. THE CKK-B
RECEPTORS OCCUR THROUGHOUT THE CENTRAL NERVOUS SYSTEM WHERE THEY
MODULATE ANXIETY, ANALGESIA, AROUSAL, AND NEUROLEPTIC ACTIVITY.
CC THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS
CC THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: STOMACH AND BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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or send an email to license@isb-sib.ch).

EMBL; D12817; BAA02250.1; -
PIR; JQ1614; JQ1614.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Lipoprotein; Palmitate.
FT DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 58 79 1 (POTENTIAL).
FT DOMAIN 80 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 150 3 (POTENTIAL).
FT DOMAIN 151 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 189 4 (POTENTIAL).
FT DOMAIN 190 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 242 5 (POTENTIAL).
FT DOMAIN 243 336 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 337 358 6 (POTENTIAL).
FT DOMAIN 359 376 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 377 397 7 (POTENTIAL).
FT DOMAIN 398 450 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 127 205 BY SIMILARITY.
FT LIPID 411 411 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 450 AA; 48755 MW; EF13BA8B5FAA857A CRC64;

Query Match 10.8%; Score 237.5; DB 1; Length 450;
Best Local Similarity 23.5%; Pred. No. 3e-09;
Matches 88; Conservative 71; Mismatches 149; Indels 67; Gaps 13;

NY6R_MOUSE STANDARD; PRT; 371 AA.

AC 061212;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Neuropeptide Y receptor type 6 (NPY6-R) (Pancreatic polypeptide receptor 2) (PP2).

DE NPY6R OR PPR2 OR NPY5R.

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=129;

RC MEDLINE=96279200; PubMed=8663568;

RX Weinberg D.H., Sirinathsinghji D.J.S., Tan C.P., Shiao L.-L., Morin N., Rigby M.R., Heavens R.H., Rapoport D.R., Bayne M.L., Casceri M.A., Strader C.D., Linemeyer D.L., Macneil D.J.; "Cloning and expression of a novel neuropeptide Y receptor."; J. Biol. Chem. 271:16435-16438(1996).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=129/Sv;

RC MEDLINE=97066971; PubMed=8910373;

RX Gregor P., Feng Y., Decarr L.B., Cornfield L.J., McCaleb M.L.; "Molecular characterization of a second mouse pancreatic polypeptide receptor and its inactivated human homologue."; J. Biol. Chem. 271:27776-27781(1996).

CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE RANK ORDER OF AFFINITY OF THIS RECEPTOR FOR PANCREATIC POLYPEPTIDES IS NPY > PYY > NPY (2-36) = [LEU-31, PRO-34] NPY > NPY (13-36) > PP. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: KIDNEY AND DISCRETE REGIONS OF THE HYPOTHALAMUS INCLUDING THE SUPRACHIASMATIC NUCLEUS, ANTERIOR HYPOTHALAMUS, BED NUCLEUS STRIA TERMINALIS, AND THE VENTROMEDIAL NUCLEUS.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.

CC -!- CAUTION: Was originally called NPY5-R.

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DR EMBL: U58367; AAB18624.1; -

DR EMBL: U59430; AAB19188.1; -

DR MGD; MGI:1098590; Npy6r.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 57 1 (POTENTIAL).

FT DOMAIN 58 69 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 70 90 2 (POTENTIAL).

FT DOMAIN 91 110 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 111 132 3 (POTENTIAL).

FT DOMAIN 133 152 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 153 174 4 (POTENTIAL).

FT DOMAIN 175 208 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 209 230 5 (POTENTIAL).

FT DOMAIN 231 261 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 262 284 6 (POTENTIAL).

FT DOMAIN 285 297 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 298 321 7 (POTENTIAL).

FT DOMAIN 322 371 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 109 196 BY SIMILARITY.

FT LIPID 336 PALMITATE (POTENTIAL).

SQ SEQUENCE 371 AA; 42713 MW; E4AAB987CEB74B7 CRC64;

Query Match 10.9%; Score 239; DB 1; Length 371;

Best Local Similarity 23.3%; Pred. No. 1.9e-09;

Matches 90; Conservative 60; Mismatches 109; Indels 128; Gaps 17;

QY 52 IVLGIGSLNLTVLVLYCMKNSVNIITMNLHVLVDVILVCIGPIPLTIVILLLS--LES 109

DB 46 LIMGIFGNLSLIIIFKKQREANQVNTILIANLSLSLILVCVMCIPTVIITLMDHWVF 105

QY 110 NTALICCFHEACVSFASVSTAI-NVFAITLDYDISVKPANRILTMGRAYMLMISWIFS 168

DB 106 NT---MCKLTSYQSVSVSVSIFSLVLIATERYQLIVNPRGKPRVAHAYWGILILWIS 162

QY 169 -----FFSFLI---PF-----IEVNFFSLQSG--NTWENK-TLLCVSTN----EYTEL 207

DB 163 LTLISIPFLSYHLTNEPFFNLSLPTDIYTHQVACVEIWPCKLNQLLSTSLFMLQYFVPL 222

QY 208 GMYVHLLVQPIFFFTVVVMLITVTKILOALNIRIGRFRSTGQKKARKKKTISLTQHE 267

DB 223 GF-----ILICYLKVLCV-----RRRT----- 240

QY 268 ATDMSSSGGRNVFVGRVTSVVIALLRAVKRHRERR---QKRVFRMSLLIISTFLL 324

DB 241 -----RQVDRKKNKSLNENKRVNVMLSIVVTFGA 272

QY 325 CWTPISVLNT-----TILCLGFSDDLVLKRLCLFLVMAYGTTTTPHLPILAFYTKQPKVL 378

DB 273 CWLPLNIFNFIIDYHEMLMSCHDLV--FVVCGLI-AMVSTCINPLFYGLNKNFKQDL 329

QY 379 KSKMKRVRVSEADPLPNNAVHNSW 405

DB 330 M-----MLIHWCW 337

RESULT 9

NY6R_RABIT STANDARD; PRT; 371 AA.

AC P79217;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Neuropeptide Y receptor type 6 (NPY6-R).

GN NPY6R.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Japanese white; TISSUE=Skeletal muscle;

RX MEDLINE=97066888; PubMed=8910290;

RA Matsumoto M., Nomura T., Momose K., Ikeda Y., Kondou Y., Akiho H., Togami J., Kimura Y., Okada M., Yamaguchi T.; "Inactivation of a novel neuropeptide Y/peptide YY receptor gene in primate species."; J. Biol. Chem. 271:27217-27220(1996).

RL J. Biol. Chem. 271:27217-27220(1996).

CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.

FT DISULFID 114 196 BY SIMILARITY.
FT LIPID 387 387 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 428 AA; 47841 MW; A6E8FABDA805E610 CRC64;
Query Match 11.5%; Score 253; DB 1; Length 428;
Best Local Similarity 22.8%; Pred. No. 2.5e-10;
Matches 95; Conservative 85; Mismatches 132; Indels 104; Gaps 18;
QY 15 SNITVRDIDDINTNMV-----QPLSYPLSFQVSLTGLMLEIVLGLSN 59
Db ||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
12 SNITPPCELGLENETFLCDQPRPSKEWQPAVQLLYSLIFLLSV-----LGNT 60
QY 60 LTVLVLCKMKNLSNIVSMNITMNLRLVDVLCVGCPIPLTIVILLLSLESNTALICCPHE 119
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
61 LVITVL--IRNKRMTVNIIFLLSLAVSDMLCLFCMPFNILPNLLKDFIGSAVC--K 115
QY 120 ACVSPASVSTAINVF---AITLDYDISVKP-ANRI-ITMGRVAVMLMISWIFSF----- 169
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
116 TTTVPMGTSVSVSTFNLVAISLERYGAICKPLQSRVMTKSHALKVIAATWCLSTIWP 175
QY 170 ---FSLPIPFIEVNFPSLQSGNTWENKTL-LC--VSTNEYTELGMVYHLLVQPIFFFT 223
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
176 YPIYSNLVFFTKNN-----NOTANMCRFLPNLV---MOQSWHTFLLLFLIP 221
QY 224 VVMLITVTKILQALNIRIGTRFSTGQKKKARKKKTISLTT-OHEATD----- 270
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
222 GIVMVAAGLI--SLELQGIKFASQKSAKERKPTSTSSGKYEDSGCYLQKTRPPRK 279
QY 271 -----MSOSSGGRNVFVGRVSVVIAALRAVKKHRRERQKRVFMSLLIISTFLLC 325
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
280 LELQRLSTGSSSRANRIRKSNSSAANLMA-----KKRVIRMLIVVIVVFLC 325
QY 326 WTPISVLTNTILCLGPSDLLVKRLC-----FLVMAYGTFIHFPLLYAFTRQFQ 375
Db ||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
326 WPIPSANA---WRAYDTASAERLSTGTPISFILLSTSSCVNPIIYCFMKNKRF 378
RESULT 7
ID CCKR_XENLA STANDARD; PRT; 453 AA.
AC P0031;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cholecystokinin receptor (CCK-XLR).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96319796; PubMed=8700154;
RA Schmitz F., Pratt D.S., Wu M.-J., Kolakowski L.F. Jr., Beinborn M.,
RA Kopin A.S.;
RT Identification of cholecystokinin-B/gastrin receptor domains that
RT confer high gastrin affinity: utilization of a novel xenopus laevis
RT cholecystokinin receptor.;
RL Mol. Pharmacol. 50:436-441(1996).
CC -1- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. THIS RECEPTOR MEDIATES ITS
CC ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A
CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. HAS HIGH
CC AFFINITY FOR CCK-8 AND LOW AFFINITIES FOR GASTRIN-17-I, CCK-4, AND
CC UNSULFATED CCK-8.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN AND STOMACH.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HAS EQUAL SIMILARITY TO TYPE A AND B CHOLECYSTOKININ MAMMALIAN
CC RECEPTORS.
CC -----
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DR EMBL; U49258; AAB09052.1; -;
DR HSP; P02699; 1F88
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Lipoprotein; Palmitate.
FT DOMAIN 1 64
FT TRANSMEM 65 94
FT TRANSMEM 95 104
FT TRANSMEM 105 131
FT TRANSMEM 132 142
FT TRANSMEM 143 164
FT TRANSMEM 165 184
FT TRANSMEM 185 205
FT TRANSMEM 206 237
FT TRANSMEM 238 261
FT TRANSMEM 262 343
FT TRANSMEM 344 364
FT TRANSMEM 365 379
FT TRANSMEM 380 403
FT DOMAIN 404 453
FT DISULFID 141 223
FT LIPID 401 401
FT CARBOHYD 9 9
FT CARBOHYD 22 22
FT CARBOHYD 30 30
FT CARBOHYD 35 35
FT CARBOHYD 39 39
SQ SEQUENCE 453 AA; 51157 MW; 06217927B7482678 CRC64;
Query Match 11.3%; Score 248.5; DB 1; Length 453;
Best Local Similarity 22.7%; Pred. No. 5.4e-10;
Matches 93; Conservative 84; Mismatches 172; Indels 61; Gaps 14;
QY 32 QPLSYPLSFQVSLTGLMLEIVLGLSNLTIVLVLYCKMKNLSNIVSMNITMNLHVLVDVII 91
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
60 KPSPDNLNLWRIVMYSVIFLLSVFGNTLIIVLYMNRK--LRTITNSFLLSLALSLDMV 117
QY 92 CVGCIPLTIVILLLSLESNTALICCFHEACVSFASVTAINVF---AITLDYDISVKP- 147
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
118 AVLCPFTLIPNLMEVFGEVIC---RAAYFMCLSVSVSTFNLVAISIERYSAINCP 174
QY 148 ANRI-LTMGRVAVMLMISWIFSFLLPIFTEVN---FFSL-----OSGNTWENKTL 196
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
175 KSRVQWTRSHAYRIAATAWTLSSIT-IMPILVYNKTVTFPMKDRRVGHCRLVWPSK--- 230
QY 197 CVSTNEYTELGMVYHLLVQPIFFFTVVMVLTITVTKILQALNIRIGTRFSTGQKKKARK 256
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
231 -----QQQAWYVLLLTILFIPGVVMIVAYGLISRELYGIQFEMDLNKEAKHK 281
QY 257 KKTISLTQHEATD-----MSOSSGGRNVFVGRVSVSVIIALRRA-VKKHRRERQKRV 311
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
282 NGVSTPTIPSGDEGDCYIQVTKRRNTMEMSTLTPSVCTKMDRARINNSEAKLMKRV 341
QY 312 FMSLLIISTELLQWTPISVLT--TILCLGPSDLLVKRLCFL-VMAYGTFIHFPLLYA 368
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
342 IRMLIVIVAMFFICWMPIFVANTWKADELAFNTLTGAPISFTHLLSYTSACVNPLIYC 401
QY 369 FTQKFKVLSKKMKRVSVIVEADPLPNNVAVIHNWDIPKRNKKTIED 418
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
402 FMNKRFRKFLGTF-----SSCIKPCRNFRDTE 431
RESULT 8

FT	TRANSMEM	366	389	7 (POTENTIAL).
FT	DOMAIN	390	444	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	25	25	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	39	39	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	129	211	BY SIMILARITY.
FT	LIPID	403	403	PALMITATE (BY SIMILARITY).
FT	SEQUENCE	444 AA;	49657 MW;	B435BE7505C2FB11 CRC64;
Query Match				
Best Local Similarity		12.2%;	Score 266.5;	DB 1; Length 444;
Matches 102; Conservative		23.8%;	Pred. No. 3.2e-11;	
			85; Mismatches 131;	Indels 111; Gaps
QY	6	I L E I N M S E S N I I T R D D I D D I N M Y	-----Q P - L S Y P L S F Q V S L T G F L M L E I V L G L S N	59
DB	18	V D S L L M N G S N I P P C E L G L E N E T F L C L D Q P Q S K E W Q A L Q I L L Y S I I F L S V L G N T I V	77	
QY	60	L T V L V L Y C M K S N L I N S V S N I I T W N L H V D I V I C V G C I P T I V I L L S L E S N T A L I C C F H E	119	
DB	78	I T V L I -----R N K R M R T V N I F L L S L A V S D I M L C L F C M P E N L P N L L K D F I F G S A V C	--K 130	
QY	120	A C V S F A S V S T A I N V F	---A T T D R Y D I S V K P - A N R I - L T M G R A V M L M I S I W I F S F	-----169
DB	131	T T T Y F M C T S V S V T F N L V A I S L E R Y G A I C R P Q S R V W Q K S H A L K V I A T W C L S T I M P	190	
QY	170	---F S P L I P P I E V N	-----F F S L Q S G ---N T W E N K T L L C V S T N E Y T E L G M Y H L L W	216
DB	191	Y P I Y S N L V P T K N N Q T A N M C R F L L P S D A M Q S Q W I F L L I	-----231	
QY	217	I P I F F T V V M L T Y Y K I L Q A L M I R I G T R F S T Q C K K A R K K - T I S L T T Q H E A T D	-----270	
DB	232	--L F L L P G I V M V A Y G L I	--S L E Y O G I K F D A Q K S A K E K P S T G S T R Y E D S D G C Y I Q	287
QY	271	-----M S O S G G R N V V G F R T S V S V	--I I A L R A V K R H R E R O K R V R M S L	316
DB	288	K S R P R K L E L Q L S S G S G S R - L N R I R S S S A A N L I A	-----K R V I R M L I	332
QY	317	L I I S T F L L C W T P I S V L N T	-----T I -----L C I G P S D L L V K L R C L F V N M A Y G T T I F H P L L	366
DB	333	V I V V L F L C W M P I F S A N A R A Y D V S A E K H L S T P I S F I	-----L L L S Y T S S C V N P I	385
QY	367	Y A F T R Q K F Q	375	
DB	386	Y C F M N K R F R	394	
RESULT 6				
ID	CCR_K_HUMAN	STANDARD;	PRT;	428 AA.
AC	P32238;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Cholestyrolin type A receptor (CCR-A receptor) (CCR-AR).			
OS	CCR AR OR CCKAR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Gall bladder;			
RX	MEDLINE=93277552; PubMed=8503909;			
RA	Ulrich C.D., Ferber I., Holicky E., Hadac E., Buell G.,			
RA	Miller L.J.;			
RT	"Molecular cloning and functional expression of the human gallbladder			
RT	cholestyrolin A receptor.";			
RL	Biochem. Biophys. Res. Commun. 193:204-211(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9343941; PubMed=8343165;			
RA	Wank S.A., de Weerth A., Pilegna J.R., Huppi K.;			
RT	"Molecular cloning, functional expression and chromosomal			

RT	localization of the human cholecystokinin type A receptor.";
RL	Biochem. Biophys. Res. Commun. 194:811-818(1993).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96029343; PubMed=7557108;
RA	Miller L.J., Holicky E.L., Ulrich C.D., Wieben E.D.;
RA	"Abnormal processing of the human cholecystokinin receptor gene in
RT	association with gallstones and obesity.";
RL	Gastroenterology 109:1375-1380(1995).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	TISSUE=peripheral blood leukocytes;
RL	MEDLINE=20145045; PubMed=10682840;
RA	Funakoshi A., Miyasaka K., Matsumoto H., Yamamori S., Takiguchi S.,
RA	Kataoka K., Takata Y., Matsue K., Kono A., Shimokata H.;
RT	"Gene structure of human cholecystokinin (CCK) type-A receptor: body
RT	fat content is related to CCK type-A receptor gene promoter
RT	polymorphism.";
RL	FEBS Lett. 466:264-266(2000).
CC	-1- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. HAS A 1000 FOLD AFFINITY
CC	FOR CCK RATHER THAN FOR GASTRIN. IT MODULATES FEEDING AND
CC	DOPAMINE-INDUCED BEHAVIOR IN THE CENTRAL AND PERIPHERAL NERVOUS
CC	SYSTEM. THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G
CC	PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC	MESSAGE SYSTEM.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
EMBL	LI3605; AAA35659.1; -
DR	EMBL; LI3605; AAA02819.1; -
DR	EMBL; U23430; AAA91123.1; -
DR	EMBL; U23427; AAA91123.1; JOINED.
DR	EMBL; U23428; AAA91123.1; JOINED.
DR	EMBL; U23429; AAA91123.1; JOINED.
DR	EMBL; D85606; BAA90879.1; -
DR	PIR; JN0590; JN0590.
DR	PIR; JN0692; JN0692.
DR	HSSP; P02699; 1F88.
DR	Genew; HGNC:1570; CCKAR.
DR	MM; 118444; -
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.
DR	PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Lipoprotein; Palmitate.
FT	DOMAIN 1 41
FT	TRANSMEM 42 67
FT	DOMAIN 68 77
FT	TRANSMEM 78 104
FT	DOMAIN 105 115
FT	TRANSMEM 116 137
FT	DOMAIN 138 157
FT	TRANSMEM 158 178
FT	DOMAIN 179 210
FT	TRANSMEM 211 234
FT	DOMAIN 235 313
FT	TRANSMEM 314 334
FT	DOMAIN 335 349
FT	TRANSMEM 350 373
FT	DOMAIN 374 428
FT	CARBOHYD 10 10
FT	CARBOHYD 24 24
FT	CARBOHYD 190 190
FT	EXTRACELLULAR (POTENTIAL).
FT	1 (POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	2 (POTENTIAL).
FT	EXTRACELLULAR (POTENTIAL).
FT	3 (POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	4 (POTENTIAL).
FT	EXTRACELLULAR (POTENTIAL).
FT	5 (POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	6 (POTENTIAL).
FT	EXTRACELLULAR (POTENTIAL).
FT	7 (POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).

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CC EMBL; AF015963; AAC07949.1; .
 DR EMBL; AF015959; AAC07949.1; JOINED.
 DR EMBL; AF015960; AAC07949.1; JOINED.
 DR EMBL; AF015961; AAC07949.1; JOINED.
 DR EMBL; AF015962; AAC07949.1; JOINED.
 DR EMBL; D85605; BAA20068.1; .
 DR HSSP; P02699; 1F88.
 DR MGD; MGI:99478; Cckar.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Lipoprotein; Palmitate.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 42 67 1 (POTENTIAL).
 FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 78 104 2 (POTENTIAL).
 FT DOMAIN 105 115 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 116 137 3 (POTENTIAL).
 FT DOMAIN 138 157 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 158 178 4 (POTENTIAL).
 FT DOMAIN 179 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 234 5 (POTENTIAL).
 FT DOMAIN 235 321 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 322 342 6 (POTENTIAL).
 FT DOMAIN 343 357 7 (POTENTIAL).
 FT TRANSMEM 358 381 7 (POTENTIAL).
 FT DOMAIN 382 436 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 437 464 8 (POTENTIAL).
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 114 196 BY SIMILARITY.
 FT LIPID 395 395 PALMITATE (BY SIMILARITY).
 FT DOMAIN 258 264 POLY-GLY.
 FT DOMAIN 265 268 POLY-SER.
 SQ SEQUENCE 436 AA; 48436 MW; EBB5D8453B792F79 CRC64;

Query Match 12.2%; Score 267; DB 1; Length 436;

Best Local Similarity 23.8%; Pred. No. 3e-11;

Matches 104; Conservative 85; Mismatches 128; Indels 120; Gaps 20;

Qy 6 ILEINMQSESNTVRDDIDDTNNM-----OP-LSYPLSFQVSLTGFLMLEIVLGLSN 59
 Db 3 VVDSLIMNGSNITPPCELGLENETLFCLDQPPQSKEMQSAVOILLYSFILLSVLGNTLV 62
 Qy 60 LTVLLVLCMKNSLNIITMNLRLVDVIVCGICPLTIVILLLESNTALICCFHE 119
 Db 63 ITVLI-----RNKMTVTNIFLLSLAVSDMLCLFCMFNLPNLKDFIGSAVC---K 115
 Qy 120 ACVSPASVSTAINVF---AITLDYDISVKP-ANRI-ITMGRAVLMISWIFSF----- 169
 Db 116 TTTVMGTSVSVSTNLVAISLERYGAICRPLQSRVQWTKSHALKVIAATWCLSTWTP 175
 Qy 170 ---FSLIPFFTEV-----FFSLQSG---NTWENKILLCVSTNEYTELMYHLLVQ 216
 Db 176 YPIYSLNLPVFTKNNQNTAMCRFLPDSAMQSQWTFLLI-----SLTQHEA 268
 Qy 217 IPIPFVTVMVLTITVKILQALNIRIGTFSTGQKKKARKKTI-----SLTQHEA 268
 Db 217 --LFLIPGVWVAVGLI--SLELTQGIKFDASQKSKAKRLSSGGGGSSSRVD 272
 Qy 269 TD-----MSQSSGGRNVTGVSFV---IALRAVRKRRHRRRERQ 308
 Db 273 SDGCVLQKSRPRKLEAQLSTSSSGGR--INRISSGAANLIA-----K 316

Qy 309 KRVRMSLLIISTFLCWTPIISVLNT-----TI-----LCLGPSLLVLYKRLCFLMAYG 358
 Db 317 KRIVMLIIVVFLCWLPIFSANAWRAYDTVSAKKHLSGTPIISFI-----LLLSYT 369
 Qy 359 TTIFHPLYAFTRQKQ 375
 Db 370 SSCVNPPIIYCFMNRFR 386
 RESULT 5
 CCKR_RAT ID CCKR_RAT STANDARD; PRT; 444 AA.
 AC P30551;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
 GN CCKAR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 111-158; 270-314 AND 392-402.
 RC TISSUE-Pancreas;
 RA MEDLINE-92212981; PubMed-1313582;
 RA Wank S.A., Harkins R., Jensen R.T., Shapira H., de Weerth A.,
 RA Slattery T.;
 RT "Purification, molecular cloning, and functional expression of the
 RT cholecystokinin receptor from rat pancreas".
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3125-3129(1992).
 CC -1- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. HAS A 1000 FOLD AFFINITY
 CC FOR CCK RATHER THAN FOR GASTRIN. IT MODULATES FEEDING AND
 CC DOPAMINE-INDUCED BEHAVIOR IN THE CENTRAL AND PERIPHERAL NERVOUS
 CC SYSTEM. THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G
 CC PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: PANCREAS AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; M88096; AAA40899.1; .
 DR EMBL; D50608; BAA09170.1; .
 DR PIR; A42685; A42685.
 DR HSSP; P02699; 1F88.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Lipoprotein; Palmitate.
 FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 57 82 1 (POTENTIAL).
 FT DOMAIN 83 92 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 93 119 2 (POTENTIAL).
 FT DOMAIN 120 130 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 131 152 3 (POTENTIAL).
 FT DOMAIN 153 172 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 173 193 4 (POTENTIAL).
 FT DOMAIN 194 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 5 (POTENTIAL).
 FT DOMAIN 250 329 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 330 350 6 (POTENTIAL).
 FT DOMAIN 351 365 EXTRACELLULAR (POTENTIAL).

QY 327 TPISLVNT-----TI-----LCLGPSDLLVLCFLVMAYGTTTFHPLLYAFTROKFO 375
 DB 329 MPISFANAWRAYDTVAERHLSGTPISFI-----LLLSYSSCVNPIIYCFMNRFR 380

RESULT 3
 CCKR_RABIT STANDARD; PRT; 427 AA.

AC 097772;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
 GN CCKAR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=95002144; PubMed=7918628;
 RA Reuben M., Rising L., Prinz C., Hersey S., Sachs G.;
 RT "Cloning and expression of the rabbit gastric CCK-A receptor.";
 RL Biochim. Biophys. Acta 1219:321-327(1994).
 CC -!- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. HAS A 1000 FOLD AFFINITY
 CC FOR CCK RATHER THAN FOR GASTRIN. IT MODULATES FEEDING AND
 CC DOPAMINE-INDUCED BEHAVIOR IN THE CENTRAL AND PERIPHERAL NERVOUS
 CC SYSTEM. THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G
 CC PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D86601; AAD11547.1; -
 DR HSP; P02699; I188.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Lipoprotein; Palmitate.
 FT DOMAIN 1 41
 FT TRANSMEM 42 67
 FT DOMAIN 68 77
 FT TRANSMEM 78 104
 FT DOMAIN 105 115
 FT TRANSMEM 116 137
 FT DOMAIN 138 157
 FT TRANSMEM 158 178
 FT DOMAIN 179 210
 FT TRANSMEM 211 234
 FT DOMAIN 235 312
 FT TRANSMEM 313 333
 FT DOMAIN 334 348
 FT TRANSMEM 349 372
 FT DOMAIN 373 427
 FT CARBOHYD 10 10
 FT CARBOHYD 24 24
 FT CARBOHYD 190 190
 FT DISULFID 114 196
 FT LIPID 366
 SEQUENCE 427 AA; 47386 MW; 089FD10E2B86DB25 CRC64;

Query Match 12.4%; Score 272; DB 1; Length 427;
 Best Local Similarity 24.8%; Pred. No. 1.3e-11;
 Matches 94; Conservative 75; Mismatches 130; Indels 80; Gaps 16;

QY 32 QPLSYPLSFQVSLTGFLMLEIVLGLGSLNLTVLVLYCMKSNLINSVSNITMNLHVLVDVII 91
 DB 44 QILLYSLIFLLSV-----LGNLTIVITVL--IRNKRMTVTNIFLLSLAISDLML 90
 QY 92 CVCGCIPLTV-ILLLSLENTALICCFHEACVSFASVS-TAINVFAITLDRDISVKP-A 148
 DB 91 CLFCMEFNLIPNLLKDFIFGSAL-CKTTYLMGTSVSVSTLNLVAISLERGAICKPLQ 148
 QY 149 NRI-LTMGRAVLMISINIFSF-----FSFLPIFIEVNFESLOSNGTWENKTLVCS 199
 DB 149 SRWQTKSHALKVIAATWCLSFALMTPPYIYSNLVPFTKN-----NOTANMCRFLP 201
 QY 200 TNEYYTELGMVYHLLVQIPIFFFTVVMLTYTKILOALNIRIGTFSGQKKARKKT 259
 DB 202 SD-----VMOQAWHTFLLLILFLIPGIVMVAYGMI--SLELYQGKIFDASQKSAKERKA 255
 QY 260 IS-----LTTQHEATDMSQSSGGRNVVFGVRTSVSVIIALRRAVKRHR 302
 DB 256 STGSGRFEDNDCYLQRSKPTROLELOQLSGGGGR--VSRIRSSSSAATLMAK----- 307
 QY 303 ERRERQKRVFRSLIISTFLCWTPTISVLNTILCLGPSDLLVKRLC-----FLVMA 356
 DB 308 -----KRVIRMLWVILFFLCWMPIFSANA---WRAYDTVSAERRLSGTPISEFILLS 358
 QY 357 YGTTTFPHLLYAFTRQKFO 375
 DB 359 YTSSCVNPIIYCFMNRFR 377

RESULT 4
 CCKR_MOUSE STANDARD; PRT; 436 AA.

ID CCKR_MOUSE
 AC 008786;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
 GN CCKAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Liver;
 RX MEDLINE=97254481; PubMed=9099891;
 RA Takata Y., Takiguchi S., Takaoka K., Funakoshi A., Miyasaka K.,
 RA Kono A.;
 RT "Mouse cholecystokinin type-A receptor gene and its structural
 RT analysis.";
 RL Gene 187:267-271(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RX MEDLINE=97396148; PubMed=9245702;
 RA Lacourse K.A., Lay J.M., Swanberg L.J., Jenkins C., Samuelson L.C.;
 RT "Molecular structure of the mouse CCK-A receptor gene.";
 RL Biochem. Biophys. Res. Commun. 236:630-635(1997).
 CC -!- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. HAS A 1000 FOLD AFFINITY
 CC FOR CCK RATHER THAN FOR GASTRIN. IT MODULATES FEEDING AND
 CC DOPAMINE-INDUCED BEHAVIOR IN THE CENTRAL AND PERIPHERAL NERVOUS
 CC SYSTEM. THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G
 CC PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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FT DOMAIN 178 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 229 5 (POTENTIAL).
 FT DOMAIN 230 315 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 316 336 6 (POTENTIAL).
 FT DOMAIN 337 370 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 350 370 7 (POTENTIAL).
 FT DOMAIN 371 433 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 425 425 R -> C (IN REF. 2).
 SQ SEQUENCE 433 AA; 49318 MW; 385868AC567C4DC1 CRC64;

Query Match 100.0%; Score 2192; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 5.2e-141;
 Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCFSPILEINMQSESNITVRDDIDINTNMYPQLSYPLSFQVSLTGLFMLEIVLGLGSL 60
 DB 1 MCFSPILEINMQSESNITVRDDIDINTNMYPQLSYPLSFQVSLTGLFMLEIVLGLGSL 60

QY 61 TVLVLYCHKSNLINSVNIITMNLHLVDVIVCGICPIPTIVILLLSLESNTALICCFHEA 120
 DB 61 TVLVLYCHKSNLINSVNIITMNLHLVDVIVCGICPIPTIVILLLSLESNTALICCFHEA 120

QY 121 CVSPASVSTAINVPAITLDYDISVKPANRLTMTGRAVLMISWIFSFSLPIPIEVN 180
 DB 121 CVSPASVSTAINVPAITLDYDISVKPANRLTMTGRAVLMISWIFSFSLPIPIEVN 180

QY 181 FFSQSGNTWENKTLVYSTNEYTELGMVYHLLVQIPIFFTVVVMVLTITKILQALNI 240
 DB 181 FFSQSGNTWENKTLVYSTNEYTELGMVYHLLVQIPIFFTVVVMVLTITKILQALNI 240

QY 241 RIGTFSTGOKKARKKKTISLTTOHEATMSQSGGRNVFVGVTSVSVIALRAVYKR 300
 DB 241 RIGTFSTGOKKARKKKTISLTTOHEATMSQSGGRNVFVGVTSVSVIALRAVYKR 300

QY 301 HREREROKRVFRMSLLIISFLICWTPIVLTITLGLPSDLLVKRLCFLVMAYGTT 360
 DB 301 HREREROKRVFRMSLLIISFLICWTPIVLTITLGLPSDLLVKRLCFLVMAYGTT 360

QY 361 IFHPLLYAFTQKFKVLSKMKRVSVIADPLPNNAVHNSWIDPKRKKITFEDE 420
 DB 361 IFHPLLYAFTQKFKVLSKMKRVSVIADPLPNNAVHNSWIDPKRKKITFEDE 420

QY 421 IREKRLVQVYTD 433
 DB 421 IREKRLVQVYTD 433

RESULT 2

CCRR_CAVPO STANDARD; PRT; 430 AA.
 AC Q63931;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
 GN CCKAR.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas, and Gall bladder;
 RX MEDLINE=94106629; PubMed=7916580;
 RA de Weerth A., Pilegna J.R., Wank S.A.;
 RT "Guinea pig gallbladder and pancreas possess identical CCK-A receptor
 subtypes: receptor cloning and expression.";
 RL Am. J. Physiol. 265:G1116-G1121(1993).
 CC -1- FUNCTION: RECEPTOR FOR CHOLECYSTOKININ. HAS A 1000 FOLD AFFINITY
 FOR CCK RATHER THAN FOR GASTRIN. IT MODULATES FEEDING AND
 DOPAMINE-INDUCED BEHAVIOR IN THE CENTRAL AND PERIPHERAL NERVOUS

CC CC SYSTEM. THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G
 CC PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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EMBL; S68242; AAB29504.1; -;
 DR HSP; P02699; IFR8.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Lipoprotein; Palmitate.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 42 67 1 (POTENTIAL).
 FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 78 104 2 (POTENTIAL).
 FT DOMAIN 105 115 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 116 137 3 (POTENTIAL).
 FT DOMAIN 138 157 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 158 178 4 (POTENTIAL).
 FT DOMAIN 179 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 234 5 (POTENTIAL).
 FT DOMAIN 235 315 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 316 336 6 (POTENTIAL).
 FT DOMAIN 337 351 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 352 375 7 (POTENTIAL).
 FT DOMAIN 376 430 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 114 196 BY SIMILARITY.
 FT LIPID 389 PALMITATE (BY SIMILARITY).
 SQ SEQUENCE 430 AA; 48210 MW; FC9F5D34032076C9 CRC64;

Query Match 12.9%; Score 282; DB 1; Length 430;
 Best Local Similarity 24.1%; Pred. No. 2.8e-12;
 Matches 101; Conservative 83; Mismatches 127; Indels 108; Gaps 19;

QY 15 SNITVRDDIDINTNMV-----QPLSYPLSFQVSLTGLFMLEIVLGLGSLN 59
 DB 12 SNITVACELGFENETLFCGLDRPRPSKEWQPAVQILLYSLIFLSV-----LGNT 60

QY 60 LTVLVLYCHKSNLINSVNIITMNLHLVDVIVCGICPIPTIVILLLSLESNTALICCFHE 119
 DB 61 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLCFMFLNPLSLKDFIFGSAYC---K 115

QY 120 ACVSFASVSTAINVFP---AITLDYDISVKP-ANRI-LTMGRAVLMISWIFSF----- 169
 DB 116 TTTTYPMTGTSVSVSTENLVSAISLERYGAICKPQSRVWQTKSHALAVIAATWCLSTWTP 175

QY 170 ---FSFLIPFTIEVNFSLQSGNTWENKTLIC--VSTNEYTELGMVYHLLVQIPIFFTV 224
 DB 176 YPIYSNLVPFTKNN---NOTGN-----MCRFLLPNDVMQOT---WHTFLLLILFLIPG 222

QY 225 VVMLITYTKILQALNIRIGTFRSTGOKKARKKKTIS-----LTTOH----- 266
 DB 223 IVMMVAYGLI--SLEYQGIKFDAIQKSAKERKTSTGSSGPMEDSDGCVLQKSRHPRKL 280

QY 267 EATDMSQSGGRNVFVGVTSVSVIALRAVYKRERREROKRVFRMSLLIISFLICW 326
 DB 281 ELRQLSPSSSGSNRINRIRSSSTANLMAK-----KRVIRMLIVLVFLCW 328

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OM protein - protein search, using sw model

Run on: December 4, 2002, 15:59:28 ; Search time 14 Seconds
(without alignments)
1282.804 Million cell updates/sec

Title: US-09-845-721-2

Perfect score: 2192

Sequence: 1 MCFSPLEINQMSSENIIVR.....ITFDESEIRKRLVQVYTD 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2192	100.0	433	1 GP22_HUMAN	Q99680 homo sapien
2	282	12.9	430	1 CCRX_CAVPO	Q63931 cavia porce
3	272	12.4	427	1 CCRX_RABIT	Q97772 oryctolagus
4	267	12.2	436	1 CCRX_MOUSE	O08786 mus musculus
5	266.5	12.2	444	1 CCRX_RAT	P30551 rattus norv
6	253	11.5	428	1 CCRX_HUMAN	P32238 homo sapien
7	248.5	11.3	453	1 CCRX_XENLA	P70031 xenopus lae
8	239	10.9	371	1 NYGR_MOUSE	Q61212 mus musculus
9	237.5	10.8	371	1 NYGR_RABIT	P79217 oryctolagus
10	237.5	10.8	450	1 GASR_PRANA	P30796 praomys nat
11	226	10.3	453	1 GASR_MOUSE	P56481 mus musculus
12	222.5	10.2	452	1 GASR_RAT	P30553 rattus norv
13	222	10.1	422	1 SHIA_HUMAN	P08908 homo sapien
14	218.5	10.0	370	1 SH5B_MOUSE	P31387 mus musculus
15	218	9.9	447	1 GASR_HUMAN	P32239 homo sapien
16	214.5	9.8	454	1 GASR_BOVIN	P79266 bos taurus
17	213.5	9.7	357	1 SH5A_RAT	P35364 rattus norv
18	213.5	9.7	452	1 GASR_RABIT	P46627 oryctolagus
19	213.5	9.7	509	1 5HT_LYMST	Q25414 lymnaea sta
20	213	9.7	453	1 GASR_CANFA	P30552 canis famli
21	212.5	9.7	460	1 OXR2_RAT	P56719 rattus norv
22	211.5	9.6	478	1 OPN4_HUMAN	Q9umh6 homo sapien
23	211	9.6	521	1 OPN4_MOUSE	Q9eqx9 mus musculus
24	210.5	9.6	373	1 GP45_MOUSE	Q9eqq4 mus musculus
25	210.5	9.6	515	1 A1AB_RAT	P15823 rattus norv
26	209.5	9.6	357	1 SH5A_HUMAN	P47898 homo sapien
27	209.5	9.6	455	1 YXAS_CAEEL	Q18179 caenorhabdi
28	208.5	9.5	370	1 SH5B_RAT	P35365 rattus norv
29	208	9.5	383	1 NYIR_CAVPO	Q9wvd0 cavia porce
30	208	9.5	383	1 NYIR_PIG	O02835 sus scrofa
31	208	9.5	515	1 A1AB_MESAU	P18841 mesocricetu
32	207	9.4	519	1 A1AB_HUMAN	P35368 homo sapien
33	206	9.4	421	1 SHIA_MOUSE	Q64264 mus musculus

34	205	9.4	423	1 SHIA_FUGRU	O42385 fugu rubrip
35	204	9.3	384	1 NYIR_HUMAN	P25929 homo sapien
36	204	9.3	457	1 DBDR_XENLA	P42290 xenopus lae
37	203.5	9.3	326	1 AAIR_BOVIN	P28190 bos taurus
38	203.5	9.3	446	1 DADR_DIDMA	P42288 didelphis m
39	203	9.3	382	1 NYIR_CANFA	O02813 canis famli
40	203	9.3	382	1 NYIR_MOUSE	Q04573 mus musculus
41	203	9.3	382	1 NYIR_RAT	P21555 rattus norv
42	202.5	9.2	444	1 OXR2_CANFA	Q9tup7 canis famli
43	202	9.2	326	1 AAIR_CANFA	P11616 canis famli
44	202	9.2	451	1 DADR_XENLA	P42289 xenopus lae
45	201.5	9.2	357	1 SH5A_MOUSE	P30966 mus musculus

ALIGNMENTS

RESULT 1

GP22_HUMAN	STANDARD;	PRT;	433 AA.
ID	Q99680; O14554;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Probable G protein-coupled receptor GPR22.		
GN	GPR22.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97225799; PubMed=9073069;		
RA	O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R.,		
RA	Heng H.H.Q., Kolakowski L.F. Jr., Lynch K.R., George S.R.;		
RT	"Cloning and chromosomal mapping of four putative novel human		
RT	G-protein-coupled receptor genes.";		
RL	Gene 187:75-81(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Gattung S.;		
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: ORPHAN RECEPTOR.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-!- TISSUE SPECIFICITY: IN THE BRAIN REGIONS FRONTAL CORTEX, CAUDATE,		
CC	PUTAMEN, AND THALAMUS; NOT IN PONS, HYPOTHALAMUS, AND HIPPOCAMPUS.		
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
EMBL	U66581; AAC51304.1; ..		
DR	EMBL: AC002381; AAB63815.1; ..		
DR	Genew; HGNC:4477; GPR22.		
DR	MIM; 601910;		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.		
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.		
FT	DOMAIN 1 45		
FT	TRANSMEM 46 66		
FT	DOMAIN 67 85		
FT	TRANSMEM 86 106		
FT	DOMAIN 107 115		
FT	TRANSMEM 116 136		
FT	DOMAIN 137 156		
FT	TRANSMEM 157 177		
FT	DOMAIN 178 198		
FT	TRANSMEM 199 219		
FT	DOMAIN 220 240		
FT	TRANSMEM 241 261		
FT	DOMAIN 262 282		
FT	TRANSMEM 283 303		
FT	DOMAIN 304 324		
FT	TRANSMEM 325 345		
FT	DOMAIN 346 366		
FT	TRANSMEM 367 387		
FT	DOMAIN 388 408		
FT	TRANSMEM 409 429		
FT	DOMAIN 430 450		
FT	TRANSMEM 451 471		
FT	DOMAIN 472 492		
FT	TRANSMEM 493 513		
FT	DOMAIN 514 534		
FT	TRANSMEM 535 555		
FT	DOMAIN 556 576		
FT	TRANSMEM 577 597		
FT	DOMAIN 598 618		
FT	TRANSMEM 619 639		
FT	DOMAIN 640 660		
FT	TRANSMEM 661 681		
FT	DOMAIN 682 702		
FT	TRANSMEM 703 723		
FT	DOMAIN 724 744		
FT	TRANSMEM 745 765		
FT	DOMAIN 766 786		
FT	TRANSMEM 787 807		
FT	DOMAIN 808 828		
FT	TRANSMEM 829 849		
FT	DOMAIN 850 870		
FT	TRANSMEM 871 891		
FT	DOMAIN 892 912		
FT	TRANSMEM 913 933		
FT	DOMAIN 934 954		
FT	TRANSMEM 955 975		
FT	DOMAIN 976 996		
FT	TRANSMEM 997 1017		
FT	DOMAIN 1018 1038		
FT	TRANSMEM 1039 1059		
FT	DOMAIN 1060 1080		
FT	TRANSMEM 1081 1101		
FT	DOMAIN 1102 1122		
FT	TRANSMEM 1123 1143		
FT	DOMAIN 1144 1164		
FT	TRANSMEM 1165 1185		
FT	DOMAIN 1186 1206		
FT	TRANSMEM 1207 1227		
FT	DOMAIN 1228 1248		
FT	TRANSMEM 1249 1269		
FT	DOMAIN 1270 1290		
FT	TRANSMEM 1291 1311		
FT	DOMAIN 1312 1332		
FT	TRANSMEM 1333 1353		
FT	DOMAIN 1354 1374		
FT	TRANSMEM 1375 1395		
FT	DOMAIN 1396 1416		
FT	TRANSMEM 1417 1437		
FT	DOMAIN 1438 1458		
FT	TRANSMEM 1459 1479		
FT	DOMAIN 1480 1500		
FT	TRANSMEM 1501 1521		
FT	DOMAIN 1522 1542		
FT	TRANSMEM 1543 1563		
FT	DOMAIN 1564 1584		
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FT	DOMAIN 1606 1626		
FT	TRANSMEM 1627 1647		
FT	DOMAIN 1648 1668		
FT	TRANSMEM 1669 1689		
FT	DOMAIN 1690 1710		
FT	TRANSMEM 1711 1731		
FT	DOMAIN 1732 1752		
FT	TRANSMEM 1753 1773		
FT	DOMAIN 1774 1794		
FT	TRANSMEM 1795 1815		
FT	DOMAIN 1816 1836		
FT	TRANSMEM 1837 1857		
FT	DOMAIN 1858 1878		
FT	TRANSMEM 1879 1899		
FT	DOMAIN 1900 1920		
FT	TRANSMEM 1921 1941		
FT	DOMAIN 1942 1962		
FT	TRANSMEM 1963 1983		
FT	DOMAIN 1984 2004		
FT	TRANSMEM 2005 2025		
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FT	TRANSMEM 2047 2067		
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FT	TRANSMEM 2089 2109		
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FT	TRANSMEM 2131 2151		
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FT	DOMAIN 2278 2298		
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FT	TRANSMEM 2341 2361		
FT	DOMAIN 2362 2382		
FT	TRANSMEM 2383 2403		
FT	DOMAIN 2404 2424		
FT	TRANSMEM 2425 2445		
FT	DOMAIN 2446 2466		
FT	TRANSMEM 2467 2487		
FT	DOMAIN 2488 2508		
FT	TRANSMEM 2509 2529		
FT	DOMAIN 2530 2550		
FT	TRANSMEM 2551 2571		
FT	DOMAIN 2572 2592		
FT	TRANSMEM 2593 2613		
FT	DOMAIN 2614 2634		
FT	TRANSMEM 2635 2655		
FT	DOMAIN 2656 2676		
FT	TRANSMEM 2677 2697		
FT	DOMAIN 2698 2718		
FT	TRANSMEM 2719 2739		
FT	DOMAIN 2740 2760		
FT	TRANSMEM 2761 2781		
FT	DOMAIN 2782 2802		
FT	TRANSMEM 2803 2823		
FT	DOMAIN 2824 2844		
FT	TRANSMEM 2845 2865		
FT	DOMAIN 2866 2886		
FT	TRANSMEM 2887 2907		
FT	DOMAIN 2908 2928		
FT	TRANSMEM 2929 2949		
FT	DOMAIN 2950 2970		
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FT	DOMAIN 2992 3012		
FT	TRANSMEM 3013 3033		
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FT	DOMAIN 3118 3138		
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FT	DOMAIN 3160 3180		
FT	TRANSMEM 3181 3201		
FT	DOMAIN 3202 3222		
FT	TRANSMEM 3223 3243		
FT	DOMAIN 3244 3264		
FT	TRANSMEM 3265 3285		
FT	DOMAIN 3286 3306		
FT	TRANSMEM 3307 3327		
FT	DOMAIN 3328 3348		
FT	TRANSMEM 3349 3369		
FT	DOMAIN 3370 3390		
FT	TRANSMEM		

A:Note: authors translated the codon MET for residue 427 as Ile, and ACC for residue 440
 C:Superfamily: vertebrate rhodopsin
 C:keywords: neurotransmitter receptor

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Query Match          9.9%; Score 216; DB 2; Length 450;
Best Local Similarity 22.0%; Pred. No. 7.3e-10;
Matches 99; Conservative 77; Mismatches 181; Indels 92; Gaps 18;

QY 8 EINMQSENIIVRDDIDDINTNMQPLSPYPLSFQVSLTG-FLMLEIVLGLGSNLTVLVLY 66
Db 5 DTTMDGEGLLVERDS-----SFRI-LTGCFLLSLILSTLLGNTLVCAAV 47

QY 67 CMKSLINSVNIIMNLHVLVDVIVCGICPLTIVILLLESNTALICCPHEAC---VS 123
Db 48 IFRHLRSKVTFVVISLAVSDLLVAVLVMFKAV-----SEIAGFWPGSFCNIWVA 100

QY 124 F---ASVTAINVFAITLDRYDISYKP--ANRILTMGRAVLMISI-WIFSFFSELIPIFI 177
Db 101 FDMCSTASILNLCVISVDRYWAISSPFYERKMT-VKAAFTIMISVANTLSVLISFIP-V 158

QY 178 EYNFFSLOSGNWE-NKTLICVSTNEYYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQ 236
Db 159 QLNWHKATTTSFLDLNASLOGISMDNCDSLNRMYAISSSLISFYIPVAIMIVTYTRIYR 218

QY 237 ALNIRIGTRFSTGOKKKARKKKTISLTQHEATDMSQSSGGGRNVVGVRTSVSVIIALRR 296
Db 219 IAQOI-RRISALERAHVAKNCQNTSGNRSSMDCQQPESNFKMSF----- 263

QY 297 AVKRREREROKRVFRMSLLIISTFLLCWTPISVLNTTI-----LCLGPS 342
Db 264 -----KRETKVLKTLVIMGVFVCCWLPFFVLNCMIPPCEPTQPSKGAEEFCINST 314

QY 343 DLLVKLRCLFLVMAYGTTIFHPLLYAFT---RQKQKVLKS-KMKKRVVSIVEADPLNN 398
Db 315 TFDV-----FIWFGWANSNLPPIIYAFNADFKAFTLLGCYRLCPMSGNAIETVSINN 369

QY 399 AVIHNSWIDPKRNKKTTFEDSEIREKRLV 427
Db 370 GAVFSSQHEPK-----GSSPRESNLV 390
  
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Search completed: December 4, 2002, 16:02:47
 Job time : 24 secs

A;Accession: JCl352
A:Molecule type: mRNA
A:Residues: 1-447 <PIS>
A:Cross-references: GB:I04473; NID:g179997; PIDN:AAA35660.1; PID:g179998
A:Experimental source: brain, gastric
R:Lee, Y.M.; Beinborn, M.; McBride, E.W.; Lu, M.; Kolakowski Jr., L.F.; Kopin, A.S.
J. Biol. Chem. 268, 8164-8169, 1993
A:title: The human brain cholecystokinin-B/gastrin receptor. Cloning and characterization
A:Reference number: A46645; MUID:93216795; PMID:7681836
A:Accession: A46645
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-447 <LEE>
A:Cross-references: GB:I08112; NID:g306488; PIDN:AAA35657.1; PID:g306489
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:129156)
R:Song, I.; Brown, D.R.; Wiltshire, R.N.; Gantz, I.; Trent, J.M.; Yamada, T.
Proc. Natl. Acad. Sci. U.S.A. 90, 9085-9089, 1993
A:title: The human gastrin/cholecystokinin type B receptor gene: alternative splice donor
A:Reference number: A48262; MUID:94022320; PMID:8415658
A:Accession: A48262
A>Status: preliminary; translated from GB/EMBL/DDBY
A:Molecule type: DNA
A:Residues: 1-447 <RES>
A:Cross-references: GB:L10822; NID:g406075; PIDN:AAC37528.1; PID:g406076
C:Genetics:
A:Gene: GDB:CKBR
A:Cross-references: GDB:136457; OMIM:118445
A:Map position: 11p15.5-11p15.4
A:introns: 51/1; 135/1; 218/2; 271/1
C:Superfamily: neurokinin 1 receptor
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone receptor
F:57-81/Domain: transmembrane #status predicted <TM1>
F:91-116/Domain: transmembrane #status predicted <TM2>
F:131-150/Domain: transmembrane #status predicted <TM3>
F:171-192/Domain: transmembrane #status predicted <TM4>
F:219-243/Domain: transmembrane #status predicted <TM5>
F:334-354/Domain: transmembrane #status predicted <TM6>
F:369-392/Domain: transmembrane #status predicted <TM7>
F:7.30.36/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:82.154.300.442/Binding site: phosphate (Ser) (covalent) #status predicted
F:127-205/disulfide bonds: #status predicted
F:321/Binding site: phosphate (Thr) (covalent) #status predicted

	Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Gaps
	9.9%; Score 218;	22.8%; Pred. No. 5e-10;	70;	Indels	92;	15;
Qy	36	YPLSFQVSLGFLMLEIVLGLSGLTLLVLVLCMKSNLSINSVTITMNLHLVDVIICVC	95			
Dd	61	YAVIFLSVSGGNMLIIIVVLGL-----SRRLRTVTFNAFLLSLVASDLLLLAVAC	107			
Qy	96	IPLTIVILLLSLENTALICCFHCAYSF-----ASTYSTAINVFATILDRIYDVSKP--A	148			
Dd	108	MPFTLLPNLMGTFTFGVIC-----KAVSYLMGVSVSVST-LSLVAIALERYSAICRPLOA	162			
Qy	149	NRIITGRAVMMLSIWIFSFESFLPIEIVNPFS-----LQSGNTWENKTLLCVSTNE	202			
Dd	163	RWQTRSHAARVIVATWLLSGL-LMVYPYTVTVQVPGRVQLQCHRWPS-----	211			
Qy	203	YYTELGMYYHLLVQIPIFFFTVVVVMILTYTKIQALNIRIGTRF-----STGQKKKARK	257			
Dd	212	--ARVRQTWSVLLLLLLLFFPGVMVAVAGLISREL--YLGLREDGSDSDSQSRVRNQ	267			
Qy	258	KTISLTQH-----EATDMQSQSGRRNVF-----GVRTSVSVIIA	293			
Dd	268	GLPGAVHQNGRCRPEETGAVGDSDCGVQVLPSPRSAPALELTALTAPGPGSGRPTQAALLA	327			
Qy	294	LRRVKRHREERQRKVFRMSLLIISTELLCTWPISVLNTTILCLGPS--DLLVKLRIC	351			
Dd	328	-----KKRVRMLLVIVLFELCLWLPVVSANTWRFAFDGGPHRAHLSGAPIS	373			
Qy	352	FL-VMAYGTTITFHPLLXYAFTRQFKQK	376			

[illegible]

Qy 329 ISVLNTTI-LCLGPSDLLVLRCLFLVMAYGTIFPHLLLYAFTRQKQKQVLRKSKMK 383
Db 361 FFVALVLPFCSSCHMPTLLGAIINWLGYSNLLNPVIYAFNKFQNFQAFKRIK 416
RESULT 11
T19135
cholecystokinin type A receptor homolog Y54E2A.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T19135; T27154
R: Smye, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19078
A:Accession: T19135
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-643 <W1>
A:Cross-references: EMBL:Z81465; PIDN: CAB03866.2; GSPDB: GNO0020; CESP: Y54E2A.1
A:Experimental source: clone C09F9
R: Lloyd, C.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20319
A:Accession: T27154
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-643 <W12>
A:Cross-references: EMBL:AL032646; PIDN: CAA21687.2; GSPDB: GNO0019; CESP: Y54E2A.1
A:Experimental source: clone Y54E2A
C:Genetics:
A:Gene: CESP: Y54E2A.1
A:Map position: 2; 1
A:Introns: 47/3; 71/2; 92/3; 170/2; 251/3; 288/2; 341/3; 428/1; 446/1; 537/2; 573/2; 603/2
Query Match 10.18; Score 222; DB 2; Length 643;
Best Local Similarity 22.2; Pred. No. 3.5e-10;
Matches 94; Conservative 86; Mismatches 188; Indels 56; Gaps 18;
Qy 2 CFSPI---LEINQSESNITVRDIDIDINTWYQPLSPFQVSLGFLMLEIVL--GL 56
Db 38 CTHPLHKYLEVCI---SRCTVPDD-----TVFFSMTDEELFEIALPGFLYLTFLVGTI 88
Qy 57 GSNLTVLVLYCMKSNLINSVNIITMNLHVDLVICVGIPLTIVILLLESNTALICC 116
Db 89 GNSWIFVWNRFKR--HRVNTNIFLASLSTADCLINFCVP----IMPKYMSHTWSMR 142
Qy 117 FHEACVS-----PASVSTAINVFAITLDYDISVKPANRI--LTMGRVNMISMISWIFS 168
Db 143 F--ACYSVHYIQQFTCFCSVLTMWTMISPERFLATAYPMRNWFESSIGRAKKVILLINWSS 200
Qy 169 FFSFLIPFIEVNF---FSLQSGNT--WENKTLICVSTNEYYTELGMYYHLVQIDIFFFTV 224
Db 201 AVLAVPTAVRMDYETNLSLSQQRVHWCRRRPPAQLGYPRTSLNKAAYVQLLLIIFPV 260
Qy 225 VMLITTTKILQALNIRIGTRFSTGQKKARKKTKTISLTQHEATDMSQSGGRNVFVG 284
Db 261 LTMSCIVARSAIVYKSKDVIISQAWFAESKAATDAVTFSGVSAIPMTTSRN----L 316
Qy 285 RTSVSVIALLRAVYKRRHRR---ERQKRVPMRSLLIISTIFLLCWTPISVLNTTILCLG- 340
Db 317 KTANTTI-----KSYSNHRNRRVAENKKQIVQMLISIVCMYTCWLP-TIVDELLTSEGY 371
Qy 341 -----PSDLLVLRCLFLVMAYGTIFPHLLLYAFTRQKQKQVLRKSKMK 391
Db 372 ICRTSNTQTLKMRMGFNALTYCOSCINPILYAFISONFRSTFTKAYSRMKSLQGVGHS 431
Qy 392 ADPL 395
Db 432 GDPL 435
RESULT 12

148231
serotonin receptor 5B - mouse
N:Alternate names: 5-hydroxytryptamine 5B receptor (5HTR-5c)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I48231
R: Matthes, H.; Boschart, U.; Amlaiky, N.; Grailhe, R.; Plassat, J.L.; Muscatelli, F.; Mol. Pharmacol. 43, 313-319, 1993
A:Title: Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors define a new
A:Reference number: 148231; MUID: 93196607; PMID: 8450829
A:Accession: I48231
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-370 <RES>
A:Cross-references: EMBL:X69867; NID: G288735; PIDN: CAA49501.1; PID: G288736
C:Superfamily: octopamine receptor type I
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; tran
Query Match 10.08; Score 218.5; DB 2; Length 370;
Best Local Similarity 23.48; Pred. No. 3.7e-10;
Matches 89; Conservative 56; Mismatches 141; Indels 95; Gaps 12;
Qy 39 SFQVSLTGFLMLEIVLGLGSLNLTVLVLYCMKSNLINSVNIITMNLHVDLVICVGIPL 98
Db 50 AFTVLVTVLLVLLIAATAFLMNLVLVT-ILVRAPHRYPHNLVASTVSDVLVAVLVNPL 108
Qy 99 TIVILL-----LSLENTALICCPHEACVSPASVSTAINVFAITLDY- 141
Db 109 SLVSEAGRRWQLGRSLRCHWISFD-----VLCC-----TASITWVAALADRYW 154
Qy 142 DISVKPANRIITMGRVNMISI-WIFFSFLPIPIEVNFESLQSGNTWENKTLICVST 200
Db 155 TITRHLQVTLTRSRASALMTATWALSALIALAPLL-----FGWGEAYDARLQRCQVS 208
Qy 201 NEYTELGMYYHLVQIDIFFFTVVMVLIITYTKILQALNIRIGTRF-----STGQKKK 253
Db 209 QE-----PSYAVESTCGAFYLPVAVLVFYWKYKAAKFRGRRRRAVPLPATTOAKE 262
Qy 254 ARKKKTSITLTQHEATDMSQSGGRNVFVGRTSVSVIALLRAVYKRRERERQKRVFR 313
Db 263 APPESEMFTARRATVTFQTS-----DSWREQEKKRAAM 298
Qy 314 MSLIISIFELCWTPISVLNTTILCLGPSDLLVLRCLG-----FLVMAYGTITRHP 364
Db 299 MVLIGLVFVLCWIPFEL-----TELISPLCACSLPPIWKSIFLWLGYSNFFNP 348
Qy 365 LLYAFTTRQKQKQVLRKSKMKR 385
Db 349 LIYTAFAKNKNYNAFKSLFTKQ 369
RESULT 13
A47430
gastrin/cholecystokinin receptor B, short splice form - human
N:Alternate names: CCK-B/gastrin receptor; cholecystokinin-B/gastrin receptor
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A47430; JCI352; A46645; A48262
R: Ito, M.; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Nakata, J. Biol. Chem. 268, 18300-18305, 1993
A:Title: Functional characterization of a human brain cholecystokinin-B receptor. A t
A:Reference number: A47430; MUID: 93352657; PMID: 8349705
A:Accession: A47430
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-447 <ITO>
A:Cross-references: GB: D13305; NID: G436039; PIDN: BAA02564.1; PID: G436040
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:136448)
R: Pisegna, J.R.; de Weerth, A.; Huppi, K.; Wank, S.A. Biochem. Biophys. Res. Commun. 189, 296-303, 1992
A:Title: Molecular cloning of the human brain and gastric cholecystokinin receptor: S
A:Reference number: JCI352; MUID: 93080572; PMID: 1280419

QY 357 YGTTTFPHLLYAFTRQKFKVLSKSM-----KKRVSVIVEADPLPNNAVHNSWID 407
Db 309 MTSIVNPLVLYFMMSKRHRALKDDMTLTNARRHTNVGLSRFTSPSVSVYRRTLE 367

RESULT 9
A46195
cholecystokinin B receptor subtype - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C:Accession: A46195
R:Wank, S.A.; Pisegna, J.R.; de Weerth, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 8691-8695, 1992
A:Title: Brain and gastrointestinal cholecystokinin receptor family: structure and function
A:Reference number: A46195; MUID:92409582; PMID:1528881
A:Accession: A46195
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-452 <WANK>
A:Cross-references: GB:M99418; NID:g203459; PIDN:AAA40925.1; PID:g203460
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:114083, NCBIP:114084)
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 10.2%; Score 222.5; DB 2; Length 452;
Best Local Similarity 22.9%; Pred. No. 2.2e-10;
Matches 87; Conservative 73; Mismatches 145; Indels 75; Gaps 12;

QY 36 YPLSFQSVLTGFLMLEIVLGLGSLNLTVLVLYCMKSNLINSVNIITMNLHVLVDVLCVGC 95
Db 61 YAVIFLMSVGGNVLIITVLGL-----SRLRTVTNFAFLLSLAVSDLLAVAC 107

QY 96 IPLTIVILLLSLESNTALICCFHEACVSF-----ASVSTAINVEATTLDRYDISVKP--A 148
Db 108 MFETLPNLMGFIETGTVIC----KAISLMGVSVSVST-LMLVALERYSAICRPLQA 162

QY 149 NRILTMGRVAMLMSIWISFSPFLIPFIEVNFSS-----LQSGTNWKNKTLILCVSTNE 202
Db 163 RVWQTRSHAARVILATWLLSLG-LMVPYPVYTMVQVPGPRVLQCMHRWFS-----211

QY 203 YTELGMYHLLVQIDIFFETVVVVMILITTKILQALNIRIGTRFSTGQKKARKKKTISL 262
Db 212 --ARVOOTWSVLLLLFPFGVIAVAYGLISRELYLGLHFHDGENDSETQSRARNQOGL 269

QY 263 TQHEATMSQSGGRNVFVGRTSVSVIILRRVAKRHRERRE-----306
Db 270 PGGAAPCPVHQGCRPV-----TSVAGEDSGCCVQLPRSRLEMTTLTPPGVPVGPGR 324

QY 307 -----ROKRVFRMSLLIISTIFLLCWTPISVINTTILCLGP--SDLLVKLRLCFL-VMA 356
Db 325 PNOAKLLAKRVVRMLLVILVFLFLCWLPVSVNTWRAFDGPGAQRALSGAPISFIHLLS 384

QY 357 YGTTTFPHLLYAFTRQKFK 376
Db 385 YVSACVNPLVYCFMHRRRFQ 404

RESULT 10
138209
serotonin receptor 1A - human
N:Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 15-May-1998 #text_change 21-Jul-2000
C:Accession: I38209; S07343; I56176; S31438
R:Jacobsen, J.S.; Refolo, L.M.; Conley, M.P.; Sambamurti, K.; Humayun, M.Z.
Mutat. Res. 179, 89-101, 1987
A:Title: DNA replication-blocking properties of adducts formed by aflatoxin B1-2,3-dichloride
A:Reference number: I38209; MUID:87258013; PMID:3110609
A:Accession: I38209
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-422 <JAC>

A:Cross-references: EMBL:X57829; NID:g36428; PIDN:CAA40962.1; PID:g36429
R:Parks, C.L.; Chang, L.S.; Shenk, T.
Nucleic Acids Res. 19, 7155-7160, 1991
A:Title: A polymerase chain reaction mediated by a single primer: cloning of genomic DNA
A:Reference number: I37104; MUID:92115564; PMID:1766875
A:Accession: I37104
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <PAR>
A:Cross-references: EMBL:Z11168; NID:g1033027; PIDN:CAA77560.1; PID:g1033028
R:Kobilka, B.K.; Frielle, T.; Collins, S.; Yang-Feng, T.; Kobilka, T.S.; Francke, U.;
Nature 329, 75-79, 1987
A:Title: An intronless gene encoding a potential member of the family of receptors co-
operates with a G protein-coupled receptor in the regulation of cyclin D1
A:Reference number: S07343; MUID:87315369; PMID:3041227
A:Accession: S07343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151, 'PR', 155-171, 'I', 173-417, 'N', 419-422 <KOB>
A:Cross-references: EMBL:X13556; NID:g35523; PIDN:CAA31908.1; PID:g35524
A>Note: the authors translated the codon ATC for residue 172 as Met
R:Aune, T.M.; McGrath, K.M.; Sarr, T.; Bombara, M.P.; Kelley, K.A.
J. Immunol. 151, 1175-1183, 1993
A:Title: Expression of 5HT1a receptors on activated human T cells. Regulation of cyclin
D1 expression by 5HT1a receptors
A:Reference number: I56176; MUID:93329096; PMID:8393041
A:Accession: I56176
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'RPR', 203-227, 'R', 229-244, 'A', 245-354, 'T', 356-362, 'MRP', <AUN>
A:Cross-references: GB:S64045; NID:9404416; PIDN:AAD13945.1; PID:94261645
C:Genetics:
A:Gene: GDB:HTR1A; ADRB2RL1; ADRBRL1
A:Cross-references: GDB:120686; OMIM:109760
A:Map position: 5cen-5q11
C:Superfamily: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter r
F:37-62/Domain: transmembrane #status predicted <TM1>
F:74-98/Domain: transmembrane #status predicted <TM2>
F:110-132/Domain: transmembrane #status predicted <TM3>
F:153-178/Domain: transmembrane #status predicted <TM4>
F:192-217/Domain: transmembrane #status predicted <TM5>
F:346-367/Domain: transmembrane #status predicted <TM6>
F:379-403/Domain: transmembrane #status predicted <TM7>
F:109-187/Disulfide bonds: #status predicted
F:420/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 10.1%; Score 222; DB 2; Length 422;
Best Local Similarity 21.9%; Pred. No. 2.2e-10;
Matches 91; Conservative 70; Mismatches 153; Indels 102; Gaps 15;

QY 38 LSPQV---SLTGFLMLEIVLGLGSLNLTVLVLYCMKSNLINSVNIITMNLHVLVDVLCVGC 94
Db 33 VSKQVITSLLLGLTFLICAVLGG---NACVNAIALESRLQN-VANYLIGSLAVTDLWVSVL 88

QY 95 CIPLTIVILLLSLESNTALICCFHEACVSFASVSPASVAINFAITLDRYDISVKPANKR--L 152
Db 89 VLPMAALYQVNLKWTGLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAITDIDYVKNR 148

QY 153 TMGRVAMLMSIWISFSPFLIPFIEVNFSLQSGTNWKNK--LLCVSTNEY-----YTE 206
Db 149 TPRRAAALISLTWLGILISIPPM-----GWRTPEDRSDPDACITSKDHGYTIYST 200

QY 207 LGMYHLLVQIDIFFETVVVVMILITTKILQALNIRIGTRFSTGQKKARKKKTISLTQH 266
Db 201 FGAFY-----IPL-----LLMVLVYGRIFRAARFRI-----RKTIVKKEVTGADTRH 242

QY 267 EATDMSQ-----SSGGRNVFVGRTSVSVIILRRVAK-----299
Db 243 GASPAQPKKSVNGESGRNWRLVGVESKAGCALCANGAVRQGDGAALIEVIEVHRVGNK 302

QY 300 -----RHRERRQRKRVFMSL-----LLISFLCWTWP 328
Db 303 EHLPLPSEAGPTPCAPASFPERKNERNAEKR--KMLARERKTVKTLGIITMGTFILCWLP 360

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Query Match 10.8%; Score 237.5; DB 2; Length 450;
Best Local Similarity 23.5%; Pred. No. 1.3e-11;
Matches 88; Conservative 71; Mismatches 149; Indels 67; Gaps 13;

Qy 36 YPLSPQVSLTGLMLEIVLGLSNLTVLVLCMKSNLINSNIITMMLHVLVDVLCVGC 95
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YAVIFLMSGNMLIIVLGL-----SRLRTVTNAPFLLSLSDLLAVAC 107

Qy 96 IPLTIVILLLESNTALICCFHEACVSF-----ASVSTAINVFATLDRYDISVKP--A 148
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 MPFTLLPLNMGTFITFGVIC-----KAVSYLMGVSVSVST-LNLVAIALERYSAICRPLQA 162

Qy 149 NRILTMGRAVLMISWIFSPFSLPIPIEVNFES-----LQSNWTWENKTLLOCVSTNE 202
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 163 RVWQTRSHARVILATWLSGL-LMVPITVTVQVGPVRLVQCMMRWPS-----211

Qy 203 YTELTGYHLLVQIPIFFFTVVMVLLTYTKILQALNIRIGTRF--SQCQKKARKKRTI 260
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 --ARVQRTQSVLLMLLFFIPGVMAVAYGLISREL--YLGRLFDGDNDSQTSVRNQG 267

Qy 261 SLTTOHEATDMSQSGGRNVGVGRTSVSVIARRA-----VKRHRER 304
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 268 GLPGCTAPCPVHONGGCRHVTAGDNDGCVQLPRSRLEMTTLTPTPGCLASANOAK 327

Qy 305 REROKRVFMSLLIISTFLLCWTPISVLTNTLILCLGPS--DLLVKRLCLFL-VMAYGTTI 361
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 328 LLAKRVVYMLLVIVLLFLLCWLPIYSANTWCAGDGPAGHRLSGAPISFILLLSYASAC 387

Qy 362 FPHLLYAFTRQKFOK 376
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 388 VNPLYVCFMHRFRQ 402

RESULT 7
JC7809
sulfakinin receptor protein, DSK-RI - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 03-Jun-2002
C:Accession: JC7809
R:Kubla, T.M.; Larsen, M.J.; Burton, K.J.; Bannow, C.A.; Martin, R.A.; Zantello, M.R.;
Biochem. Biophys. Res. Commun. 291, 313-320, 2002
A:Title: Cloning and functional expression of the first Drosophila melanogaster sulfakinin
A:Reference number: JC7809; PMID:11846406; MUID:21835488
A:Accession: JC7809
A:Molecule type: mRNA
A:Residues: 1-584 <KUB>
A:Cross-references: GB:AX128640
C:Comment: This receptor, the first functionally active orphan Drosophila sulfakinin G-P
nctions.
C:Genetics:
A:Gene: dsk-rl
A:Map position: 17
F:115-139/Domain: transmembrane region #status predicted <TMR1>
F:149-167/Domain: transmembrane region #status predicted <TMR2>
F:189-207/Domain: transmembrane region #status predicted <TMR3>
F:229-250/Domain: transmembrane region #status predicted <TMR4>
F:275-300/Domain: transmembrane region #status predicted <TMR5>
F:431-454/Domain: transmembrane region #status predicted <TMR6>
F:467-491/Domain: transmembrane region #status predicted <TMR7>

Query Match 10.5%; Score 229.5; DB 2; Length 584;
Best Local Similarity 20.4%; Pred. No. 7.7e-11;
Matches 88; Conservative 86; Mismatches 153; Indels 105; Gaps 14;

Qy 33 PLSVPLSFQVSLTG-----FLMLEIVLGLSNLTVLVLCMKSNLINSNIITMNL 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 96 PSSPTASSSTSTGMPWMLIPSYSMILLFAVLGNLLVISTL--VQNRRTIRITNVFLLN 153

Qy 85 HVLVDVLCVGCPIPLTIVILLLESNTALICCFHEACVSFASVSTAINVFATLDRYDIS 144
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 154 AISDMLGLVCMPTLVGTLNRFIFGFLCKLQFSQAASAVSVSSWTLVAISCERYAI 213
```

```
Qy 145 VKP--ANRILTMGRAVLMISWI-----FSFSLPIPIEVNFESLOSNTWENKT 194
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 CHPLRSRQWQITSHAYKIIGFIWLGILCMTPDIAVFSOLIPSTRPGY-----260

Qy 195 LLCVSTNEYTELG--MYTHLIVQIPIFFFTVVMVLLTYTKILQALNI-----RI---242
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 261 --CKREFWPDQGVLEFYNILLDFLLVPLPLVCVAILITRLYVGMAKDSGRILQQ 317

Qy 243 -----GTRFST-----GQKKARKK 257
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 318 SLPVSATTAGGAPNPGTSSSNICILVTATAVYNNNSNNNGNSEGSAGGSGTNMA---374

Qy 258 KTSILTTOHEATDMSQSGGRNVGVGRTSVSVII--ALRRAVHRHREKRVFRM 314
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 375 -TTTTLTPTAPTATVTTTTTTTTLAKTSSPSIRVHDAALRNS--NEAKTLESKRVVKM 431

Qy 315 SLLIISTFLLCWTPISVLTNTLILCLGP--SDLLVKRLCLFL-VMAYGTTIFHPLLYAFTR 371
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 432 LFVLVLEFFICWTPVLTNTVWMLIGPVVYEVVDYTAISFLOLLAYSSCCNPITYCPMN 491

Qy 372 QKFQVLSKMK 383
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 492 ASFRFAFVDTEK 503

RESULT 8
T27559
hypothetical protein ZC412.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27559
R:Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z20387
A:Accession: T27559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-539 <WIL>
A:Cross-references: EMBL:Z78067; PIDN:CA801528.1; GSPDB:GN00023; CESP:ZC412.1
A:Experimental source: clone ZC412
C:Genetics:
A:Gene: CESP:ZC412.1
A:Map position: 5
A:Introns: 29/3; 75/3; 112/1; 144/3; 180/3; 223/3; 241/3; 324/3; 376/2; 426/2; 456/3

Query Match 10.2%; Score 224; DB 2; Length 539;
Best Local Similarity 21.2%; Pred. No. 2e-10;
Matches 89; Conservative 82; Mismatches 150; Indels 98; Gaps 14;

Qy 25 DINTNMQPLSYPLSFQVSLTGFLMLE---IVLGLSNLTVLVLCMKSNLINSVSNIT 81
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 DVNAILQOFNDWTVLFEVRL-GYSVLYFLIILIGLVGNGLLITSLMRKKL--SVANIFL 67

Qy 82 MNLHVLVDVLCVGCPIPLTIVILLLESNTALICCFHEACVSFASVSTAINVFATLDRY 141
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 INLAVSDLLCLITAVPIPTPLAFMKRWTFITMCKLVPTCOAFSVLLISLICYAIDRY 127

Qy 142 DISVKPANRILTMGRAVLMISWIFSPFSLPIPIEVNFESLOSNTWENKTL---LC- 197
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 RSIVTPLREPWSDRHARWLMFTVWVAFSLASPLYSYSLNLTMTM-----VIENVTLGDFCG 183

Qy 198 -----VSTNEYTELGMYYHLVQIPIFFFTVVMVLLTYTKILQALNIRIGTRFSTG 249
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 184 EFNQSDSEIKLTYTSL-----LIQLII--PAIMSFVCLMILQVQ-----225

Qy 250 QKKARKKKTLILTQHEATDMSQSGGRNVGVGRTSVSVIILRAVAKHRERRERQK 309
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 -----TDWLVEG-----SMLTAAQA-----QTAVRKR 249

Qy 310 RVFRMSLLIISTFLLCWTPISVLTNTLILCLGPSDLLVKRLCLFLVMA 356
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 RVMYVLILMVIVFACWFLSAVNLFRDLGMRFEFCQVYKVLMMQMYFKL-LNVHVIA 308
```

F:57-82/Domain: transmembrane #status predicted <TM1>
F:93-119/Domain: transmembrane #status predicted <TM2>
F:131-151/Domain: transmembrane #status predicted <TM3>
F:171-193/Domain: transmembrane #status predicted <TM4>
F:225-249/Domain: transmembrane #status predicted <TM5>
F:330-348/Domain: transmembrane #status predicted <TM6>
F:366-389/Domain: transmembrane #status predicted <TM7>

Query Match 12.2%; Score 266.5; DB 2; Length 444;
Best Local Similarity 23.8%; Pred. No. 5.8e-14;
Matches 102; Conservative 85; Mismatches 131; Indels 111; Gaps 20;

QY 6 ILEINMQSNTIVRDDIDDINTNMV-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59
DB 18 VVDSLMLNGSNITPPCELGLENETLFCLDQPPQSKWQALQILLYSIIFLLSVLGNLV 77
QY 60 LTVLVLYCMKSNLINSVNIITMNLHVLDVVICGVCPIPTIVILLLSLESNTALICCFHE 119
DB 78 IIVLI-----RNKRMRTVTNIFLLSLAVSDLMCLFCMPENLPNLLKDFIFGSAVC---K 130
QY 120 ACVSFASVSTAINVF---AITLDYDISVKP-ANRI-LTMGRAVMLMISIWIFSF----- 169
DB 131 TTTYFMGTSVSTENFVAISLERYGAICRPLQSRVWQTKSHALKVIAATWCLSFMTMP 190
QY 170 ---FSLFPIEFVW-----FPSLSQ---NWNKNTLLCVSTNEYYTELGMYHLLVQ 216
DB 191 YPIYSNLVFPFTKNNOTANMCRFLPDSAMQOSWQTFLLI----- 231
QY 217 IPIFEFTVVMLTYTKILQALNIRIGTRFSTGQKKARKKK-TISLTTOHEATD----- 270
DB 232 --LFLPLGVIMVAYGLI--SLEYQGIKFDASQKSAKEKPPSTGSTRYEDSDGCIYQ 287
QY 271 -----MSQSSGGNNVFGVRTSVSV---IIALRAVRKRRRERQKRVFRMSL 316
DB 288 KSRRPRKLELQQLSSGSGGR-LNRRSSSSAANLTA-----KKRVIRMLI 332
QY 317 LIISTFELLQWTPISVNT-----TI-----LCIGPSDLLVKRLCLFLVMAYGTTIFHP 366
DB 333 VIVVLEFLQWMPITFSANAWRAVDTVAEKHLGTPISFI-----LLLSYSSCVNPII 385
QY 367 YAFTRQKQF 375
DB 386 YCFMNRFR 394

RESULT 5
JN0692
cholecystokinin type A receptor - human
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C:Accession: JN0692; JN0590
R:de Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A.
Biochem. Biophys. Res. Commun. 194, 811-818, 1993
A:Title: Molecular cloning, functional expression and chromosomal localization of the hu
A:Reference number: JN0692; MUID:93343941; PMID:8343165
A:Accession: JN0692
A:Molecule type: mRNA
A:Residues: 1-428 <DEW>
A:Cross-references: GB:L19315; NID:q306595; PIDN:AAA02819.1; PID:q306596
A:Experimental source: gallbladder
R:Ulrich, C.D.; Ferber, I.; Hollicky, E.; Hada, E.; Buell, G.; Miller, L.J.
Biochem. Biophys. Res. Commun. 193, 204-211, 1993
A:Title: Molecular cloning and functional expression of the human gallbladder cholecysto
A:Reference number: JN0590; MUID:93277552; PMID:8503909
A:Accession: JN0590
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-428 <ULR>
A:Cross-references: GB:L13605; NID:q306490; PIDN:AAA35659.1; PID:q306491
A:Experimental source: gallbladder
C:Comment: This protein has diverse physiological roles in the gastrointestinal system w
ch, and secretion from gastric mucosal cells.
C:Genetics:

A:Gene: GDB:CKAR
A:Cross-references: GDB:141927; OMIM:118444
A:Map position: 4pter-4qter
C:Superfamily: G protein-coupled receptor
F:40-67/Domain: transmembrane #status predicted <TM1>
F:78-104/Domain: transmembrane #status predicted <TM2>
F:116-137/Domain: transmembrane #status predicted <TM3>
F:158-178/Domain: transmembrane #status predicted <TM4>
F:208-234/Domain: transmembrane #status predicted <TM5>
F:314-332/Domain: transmembrane #status predicted <TM6>
F:350-369/Domain: transmembrane #status predicted <TM7>
F:10,24,190,299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:245,249,260,290/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #sta
F:256/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predi

Query Match 11.5%; Score 253; DB 2; Length 428;
Best Local Similarity 22.8%; Pred. No. 6.9e-13;
Matches 95; Conservative 85; Mismatches 132; Indels 104; Gaps 18;

QY 15 SNITVRDDIDDINTNMV-----OPLSYPLSFQVSLTGFLMLEIVLGLGSN 59
DB 12 SNITPPCELGLENETLFCLDQPPRPSKEWQPAVQILLYSLIFLSV-----LGNT 60
QY 60 LTVLVLYCMKSNLINSVNIITMNLHVLDVVICGVCPIPTIVILLLSLESNTALICCFHE 119
DB 61 LVITVL--TRNKRMTVTNIFLLSLAVSDLMCLFCMPENLPNLLKDFIFGSAVC---K 115
QY 120 ACVSFASVSTAINVF---AITLDYDISVKP-ANRI-LTMGRAVMLMISIWIFSF----- 169
DB 116 TTTYFMGTSVSTENFVAISLERYGAICRPLQSRVWQTKSHALKVIAATWCLSFMTMP 175
QY 170 ---FSLFPIEFVWTFSLQSGNTWENKTL-LC--VSTNEYYTELGMYHLLVQIPIFFFT 223
DB 176 YPIYSNLVFPFTKNN-----NOTANMCRFLPNDV---MQOSWHTFLLILFLIP 221
QY 224 VVMLTYTKILQALNIRIGTRFSTGQKKARKKKTISLT-TOHEATD----- 270
DB 222 GIVMVAAYGLI--SLEYQGIKFEASQKSAKERRKSTSSGKYEDSDGCIYQAKTRPRK 279
QY 271 -----MSQSSGGNNVFGVRTSVSVIIALRAVRKRRERQKRVFRMSLIIISTFLLC 325
DB 280 LELRQLSTGSSSRANRIRSNSSAANLMA-----KKRVIRMLIVIVLFFLC 325
QY 326 WTPISVLTNTILCLGPSDLLVKRLC-----FLVMAYGTTIFHPLLYAFTRQKQF 375
DB 326 WMPIFSANA--WRAYDTASAERRLSGTPISFILLISYSSCVNPIIYCFMNRFR 378

RESULT 6
JQ1614
gastrin receptor - multimammate rat (Mastomys natalensis)
C:Species: Mastomys natalensis
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000
C:Accession: JQ1614
R:Nakata, H.; Matsui, T.; Ito, M.; Taniguchi, T.; Naribayashi, Y.; Arima, N.; Nakamur
Biochem. Biophys. Res. Commun. 187, 1151-1157, 1992
A:Title: Cloning and characterization of gastrin receptor from ECL carcinoma tumor of
A:Reference number: JQ1614; MUID:92412082; PMID:1530611
A:Accession: JQ1614
A:Molecule type: mRNA
A:Residues: 1-450 <NAK>
A:Cross-references: GB:D12817; NID:q220646; PIDN:BAA02250.1; PID:q220647
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane
F:59-83/Domain: transmembrane #status predicted <TM1>
F:87-109/Domain: transmembrane #status predicted <TM2>
F:132-150/Domain: transmembrane #status predicted <TM3>
F:172-188/Domain: transmembrane #status predicted <TM4>
F:216-243/Domain: transmembrane #status predicted <TM5>
F:334-357/Domain: transmembrane #status predicted <TM6>
F:380-398/Domain: transmembrane #status predicted <TM7>
F:7,30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted

gastric CCK-A receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000

C:Accession: S50150

R:Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.

Biochem. Biophys. Res. Commun. 1219, 321-327, 1994

A:Title: Cloning and expression of the rabbit gastric CCK-A receptor.

A:Reference number: S50150; MUID:95002144; PMID:7918628

A:Accession: S50150

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-427 <RED>

C:Superfamily: neurokinin 1 receptor

Query Match 12.2%; Score 268; DB 2; Length 427;

Best Local Similarity 24.3%; Pred. No. 4.2e-14;

Matches 92; Conservative 76; Mismatches 131; Indels 80; Gaps 15;

Qy 32 OPLSYPLSFQVSLTGFLMLEIVLGLSNTLVLVLCMSKNSLINSVSNITMNLHLVDVII 91

Db 44 QILLYSLIFLSV-----LGNLTIVTVL--IRNKRMTVTNIFLISLSDML 90

Qy 92 CVGCIPLTIV-ILLLSLSENALICCFHEACVSFASV-TAINFAITLDYDISVKP-A 148

Db 91 CLFCMPENLIPNLKDFIGSAL--CKTTVLMGTSVSVSTNLVAISLERYGAICKPLQ 148

Qy 149 NRI-LTMGRVAVMLMSIWFSF-----PSFLIPFTEVNFSSLOSGNTWENKTLTLCVS 199

Db 149 SRVMTQSHALKVIAATWCLSFATMTPPIYSNLVPPFTKN-----NOTANMCRFLLP 201

Qy 200 TNEYTELGMVYHLLVQIPIFFETVVVMLITVTKILOALNIRIGTFSTGOKKARKKKT 259

Db 202 SD-----VMQQAHTFLILLIFLIPGVMMVAYGMI--SLELYQGKIFDASOKKSAKKA 255

Qy 260 IS-----LTTQHEATDMSQSSGGRNVVFGVTSVSVIIALRRVAKRHR 302

Db 256 STGSRFEDNGCYLQSKPTROLELOQLSGGGGRVSRHSSSAAALMA----- 306

Qy 303 ERREQRKRVFMSLLIITFLCWTPIPSVLNTTILCLGSPDLLVKRLC-----FLVMA 356

Db 307 -----KKRVIRMLVIVVFLFCWMPIFSANA---WRAIDTVSAERRLSGTPIPSIFLLLS 358

Qy 357 YGTTIFHPLLYAFTROKFO 375

Db 359 YTSSCVNPIIYCFMKNRFR 377

RESULT 3

cholecystokinin-A receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Apr-2000

C:Accession: JC5599

R:Lacourse, K.A.; Lay, J.M.; Swanson, L.J.; Jenkins, C.; Samuelson, L.C.

Biochem. Biophys. Res. Commun. 236, 630-635, 1997

A:Title: Molecular structure of the mouse CCK-A receptor gene.

A:Reference number: JC5599; MUID:97396148; PMID:9245702

A:Accession: JC5599

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-436 <LAC>

A:Note: translation not complete

C:Comment: This receptor belongs to the seven transmembrane G-protein coupled receptor 1

der contraction, and cholecystokinin inhibition of food intake.

C:Superfamily: neurokinin 1 receptor

F:42-67/Domain: transmembrane #status predicted <TM>

Query Match 12.2%; Score 267; DB 2; Length 436;

Best Local Similarity 23.8%; Pred. No. 5.2e-14;

Matches 104; Conservative 85; Mismatches 128; Indels 120; Gaps 20;

Qy 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Db 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Qy 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Db 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Qy 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Db 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Qy 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Db 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Qy 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Db 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Qy 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Db 6 ILEINMQSESNTVRRDDIDNTNMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLGSN 59

Db 3 VVDSLLMNGSNITPPCELGLENETLFCLDQPOPSKEWQSAVOILLYSFILLVGLNTLV 62

Qy 60 LTVLVLYCMKSNLINSVSNITMNLHLVDIIVCGICPLTIVILLLSLESNTALICCPHE 119

Db 63 ITVLII-----RNKRMTVTNIFLLSLAVSDMLCLFCMPFNLPNLLKDFIGSAVC--K 115

Qy 120 ACVSPASVSTAINVP--AATLDYDISVKP-ANRI-LTMGRVAVMLMSIWFSF----- 169

Db 116 TTTYFMGTSVSVSTPNLVVAISLERYGATCRPQSQRWQTKSHALKVIAATWCLSFITMP 175

Qy 170 ---FSFLIPFIEVN-----FFSLQSG---NTWENKTLICVSTNEYXTLGMVYHLLVQ 216

Db 176 YPIYSNLVPTFKNNQNTANMCRFLLPDSAMQSQSWQTFLLI----- 216

Qy 217 IPIFFTVVVMILITVTKILOALNIRIGTFSTGOKKARKKKTII-----SLTQHEA 268

Db 217 --LFLIPGVMMVAVGLI--SLELYQGKIFDASOKKSAKRLSSGGGGGSSSRVED 272

Qy 269 TD-----MSQSSGGRNVVFGVTSVSV--IIALRRVAKRHRERRO 308

Db 273 SDGCYLOKSRPRKLELOQLSTSSSGGR--INRIKSSGSAANLIA-----K 316

Qy 309 KRVRMSLLIISTFLLCWTPIPSVLNT-----TI-----LCLGSPDLLVKRLCFLVMAYG 358

Db 317 KRVRMLVIVVFLFCWMPIFSANRAYDITVSAEKLHSLGTPISFI-----LLLSYT 369

Qy 359 TTIFHPLLYAFTROKFO 375

Db 370 SSCVNPPIIYCFMKNRFR 386

RESULT 4

A42685

cholecystokinin receptor type A - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000

C:Accession: A42685; JC4225; PC2213

R:Wank, S.A.; Harkins, R.; Jensen, R.T.; Shapira, H.; de Weerth, A.; Slattery, T.

Proc. Natl. Acad. Sci. U.S.A. 89, 3125-3129, 1992

A:Title: Purification, molecular cloning, and functional expression of the cholecysto

A:Reference number: A42685; MUID:92212981; PMID:1313582

A:Accession: A42685

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-444 <WAN>

A:Cross-references: GB:M88096; NID:g203383; PIDN:AAA40899.1; PID:g203384

A:Experimental source: pancreas

A:Note: sequence extracted from NCBI backbone (NCBI:93814, NCBI:93815)

R:Takata, Y.; Takiguchi, S.; Funakoshi, A.; Kono, A.

Biochem. Biophys. Res. Commun. 213, 958-966, 1995

A:Title: Gene structure of rat cholecystokinin type-A receptor.

A:Reference number: JC4225; MUID:95382845; PMID:7654260

A:Accession: JC4225

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-223 <TAK>

A:Cross-references: DBJ:D50608; NID:g1100752

R:Mantamadiotis, T.; Baldwin, G.S.

Biochem. Biophys. Res. Commun. 201, 1382-1389, 1994

A:Title: The seventh transmembrane domain of gastrin/CCK receptors contributes to non

A:Reference number: PC2213; MUID:94296413; PMID:8024583

A:Accession: PC2213

A:Status: preliminary

A:Molecule type: protein

A:Residues: 366-389 <MAN>

C:Comment: This G-protein-coupled receptor is present in the gastrointestinal system,

4, smooth muscle contraction of the gallbladder and stomach. It is capable of activati

ducing the subsequent release of intracellular calcium.

C:Genetics:

A:Gene: CCKAR

A:Introns: 53/1; 137/1; 224/2; 267/1

C:Superfamily: neurokinin 1 receptor

C:Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	282	12.9	430	2	I51898	cholecystokinin A
2	268	12.2	427	2	S50150	gastric CCK-A rece
3	267	12.2	436	2	JC5599	cholecystokinin A
4	266.5	12.2	444	2	A42685	cholecystokinin re
5	253	11.5	428	2	JN0692	cholecystokinin ty
6	237.5	10.8	450	2	JQ1614	gastrin receptor -
7	229.5	10.5	584	2	JC7809	sulfakinin recepto
8	224	10.2	539	2	T27559	hypothetical prote
9	222.5	10.2	452	2	A46195	cholecystokinin B
10	222	10.1	422	2	I38209	serotonin receptor
11	222	10.1	643	2	T19135	cholecystokinin ty
12	218.5	10.0	370	2	I48231	serotonin receptor
13	218	9.9	447	2	A47430	gastrin/cholecysto
14	217	9.9	580	2	H87963	protein I54E2A.1 (
15	216	9.9	450	2	A55886	dopamine receptor
16	214	9.8	369	2	S38744	serotonin receptor
17	213.5	9.7	357	2	B47472	5-hydroxytryptamin
18	213.5	9.7	452	2	JC2459	gastrin/cholecysto
19	213.5	9.7	509	2	A47174	serotonin receptor
20	213	9.7	453	2	S32817	gastrin receptor -
21	210.5	9.6	357	2	S28058	serotonin receptor
22	209.5	9.6	357	2	I37107	5-HT5A serotonin r
23	209.5	9.6	409	2	I48095	A2 adenosine recep
24	209.5	9.6	455	2	T15622	hypothetical prote
25	208	9.5	515	2	A40491	alpha-1-adrenergic
26	207.5	9.5	517	2	A45121	alpha-1B adrenergic
27	206.5	9.4	326	2	A38144	adenosine receptor
28	206	9.4	421	2	I49375	serotonin receptor
29	204	9.3	384	2	A45490	neuropeptide Y/pep

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[illegible]

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RESULT 15
US-10-044-592-74
; Sequence 74, Application US/10044592
; Patent No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Fukusumi, Shoji
; TITLE OF INVENTION: Polypeptides, their Production and Use

```

```

; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 74
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-592-74

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Query Match 8.8%; Score 193.5; DB 12; Length 370;
Best Local Similarity 20.9%; Pred. NO. 2.9e-10;
Matches 76; Conservative 66; Mismatches 119; Indels 103;

[illegible]

Qy	145	VKPNRILTMGRAVMLMISIWISFSPFLPFTEVNFESLOSNGNTWENKTILCV----	STN	201
		: : : : :		
Db	164	VHPLRRIRLSLAYATIALWALSVALPAAYHTYHVELK-----PHDVRICEEFWGSG	218	
		: : : : :		
Qy	202	EYTELGMVYHLLVQIPIPEFTVVVMILTITKTLQALNIRIGTFSTGQKKARKKKTIS	261	
		: : : : :		
Db	219	ERQQLYAWGLLV--TYLLPLIVILLSRVV-----SVKLNRNVDPG	259	
		: : : : :		
Qy	262	LTTQHEATDNMQSSGGNNVFGVRTSVSVIIALRAVKRHREERRQRKVFRMSLLIIST	321	
		: : : : :		
Db	260	CVTQSQA-DWD-----RARRRTFCLLVVVVVV	286	
		: : : : :		
Qy	322	FLLCWTDISVLNTLILCLGPSDL-----LVKLRLCYLMAYGTITFHPLLAFYAPTKQEQ	375	
		: : : : :		
Db	287	FAVCWLPEHFVN-LLRDLDPHAIDPYAGFLVOL-LCHW-LAMSSACYNPFIYAWUHDSFR	343	
		: : : : :		
Qy	376	KVLK	379	
		: : : : :		
Db	344	EELR	347	
		: : : : :		

Search completed: December 4, 2002, 16:03:31
Job time : 14 secs

Db 277 SPEKVLMDGSRKDKALPNSGDETLN--RRSTST-----IGKKSQVTSNEQORASKVL 326
QY 316 LLIISTELLCTWTPISVLN--TTILCLGPSDLLVKKRL--CFLVMAYGTTIFHPLLYAFTRQK 373
Db 327 GIVFFLLMWCPPFITNITLVLCDSQNTTQMLLEIFWVGVSQVNPVLYTLENKT 386
QY 374 FQ-----KVLKS--KMKKRVVSIVEADPLPNNAV-----IHNS-----WIDPK 409
Db 387 FRDAGRYITCNVRSKVTLRSSKIYFRNPMASNFKKKHGRNGINPAMYQSPM 446
QY 410 RNKKITFEDSEI 421
Db 447 RLRSSTIQSSSI 458
RESULT 12
US-09-919-497-72
; Sequence 72, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 72
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-72

Query Match 8.9%; Score 195; DB 10; Length 481;
Best Local Similarity 20.8%; Pred. No. 3e-10;
Matches 90; Conservative 83; Mismatches 167; Indels 92; Gaps 19;

QY 48 LMLEIVGLGSNLTVLVLYCKMSNLINSVNIITPMNLHVLVDVLCVGCIPLTIVILLLSL 107
Db 61 ILMWIITGIGTTLVILAVSLKKL-QYATNYFLMSLAVADLLVGLFVMPALTITMFEA 119
QY 108 ESNTALICC---PHEACVSFASVSTAINVFAITLDYDISVKP--ANRILTMGRVYMLM 161
Db 120 MWPLVLCFANLFDLVLFSTASI---MHLCAISVDYVIAIKKPIQANQYNSRATAFIKI 176
QY 162 ISIWIFSFSLPIEFIEVNFPSLQSGNTWENKTLTLCVSTNEYTELGMYYHLLVQIPFIFF 221
Db 177 TVVWLIS-IGTAIP-VPIKGIETDVDPN---NNITCVLTKEREGD---FMLFGSLAAPP 227
QY 222 FTVVVMLITTKILOALNIRIGTRFSTGQKKKARKK-----TISLTTQHEATDMS 272
Db 228 TPLAIMIVTYFLTHAL-----QKAVLVKNKPPQRLTWLTVSTVFQDETPCS 276
QY 273 Q-----SSGGRNVFSGVTSVSIILALRRVAKRHRERQKRVFRMS 315
Db 277 SPEKVLMDGSRKDKALPNSGDETLN--RRSTST-----IGKKSQVTSNEQORASKVL 326
QY 316 LLIISTELLCTWTPISVLN--TTILCLGPSDLLVKKRL--CFLVMAYGTTIFHPLLYAFTRQK 373
Db 327 GIVFFLLMWCPPFITNITLVLCDSQNTTQMLLEIFWVGVSQVNPVLYTLENKT 386
QY 374 FQ-----KVLKS--KMKKRVVSIVEADPLPNNAV-----IHNS-----WIDPK 409
Db 387 FRDAGRYITCNVRSKVTLRSSKIYFRNPMASNFKKKHGRNGINPAMYQSPM 446
QY 410 RNKKITFEDSEI 421
Db 447 RLRSSTIQSSSI 458
RESULT 13

US-09-804-551B-8
; Sequence 8, Application US/09804551B
; Patent No. US20020056151A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Receptors for peptides from insects
; FILE REFERENCE: Le A 34 394
; CURRENT APPLICATION NUMBER: US/09/804,551B
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: DE 100 13 618.4
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-804-551B-8

Query Match 8.9%; Score 195; DB 10; Length 518;
Best Local Similarity 21.2%; Pred. No. 3.3e-10;
Matches 81; Conservative 66; Mismatches 129; Indels 106; Gaps 13;
QY 53 VLGIGSNLTVLVLY-CMKSNLINSVNIITMNLHVLVDVLCVGCIPLTIVILLLSLSNT 111
Db 75 VLVFGN--VLVCYVLRNRAMQTVNIFITNLALSDILLCVLAVPFTPLVTFMGRWAFG 132
QY 112 ALIC---CFHEACVSFASVSTAINVFAITLDYDISVKPANRILTMGRVYMLMISWIFS 168
Db 133 RSLCHLVSAQGCISYISTLT---LTSIAIDRYEVIYFPHPMKLSTCIGIIVSIWIA 189
QY 169 FFSFLPIEFIEVNFPSLQSGNTWENKTLTLCVSTNEYTELGMYYHLLVQIPFIFFTVVVM 228
Db 190 LLA-TVPPY-----GMYKMTNELVNGTQTGNETL 217
QY 229 ITYTKILOALNIRIGTRFSTGQKKKARKKKTISLTTQHEATDMSQSGGRNV----- 280
Db 218 VEATLMLNGSFVAQSGFIEAPDSTS-----ATQAYMQVMTAGSTGPEMPYRVYCE 269
QY 281 -----VFGVRS-----VSIIALR-----RAVKRHRER 306
Db 270 ENWPFSEQYRVFGAITTLQFVLPFFIISICVWISVKLNQARAKPCKSSRREEDRD 329
QY 307 ROKRVFMSLLIISTFLCTWTPISVLNITLCLGPSDLLVKLR-----LCFLV---MAY 357
Db 330 RKRTRNMLIAMVAVFGLSWLPINNVNIF-----DDFDDKSNEWRFYILFFVFAHSIAM 383
QY 358 GTTIFHPLLYAFTRQKFKVLK 379
Db 384 SSCYCNFPLIWLNLNENFRKEFK 405

RESULT 14
US-10-044-592-12
; Sequence 12, Application US/10044592
; Patent No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; TITLE OF INVENTION: Polypeptides, their production and use
; FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR APPLICATION NUMBER: PCT/JP98/01923
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: JP 9-109974
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 12
; LENGTH: 370

Db 3 DYNSTINLSRTRVLAFFMSLVAP---AIMLG---NALVILAFVVDKNLRH--SSYFPL 55
Qy 83 NLHVLVDVIVCGICPILVILLLESNTALICCFHEACVSPASVSTAINVFAITLDRYD 142
Db 56 NLAISDFVGVISIPLYPHITLFEWDEGKE-ICVFWLTDYLLCTASVYNIVLISYDRY- 113
Qy 143 ISVKPANRILTMGRVAVM---LMSIWIFSPFSLIPFIEVNFSSQSGNTWENKTLICV 198
Db 114 LSVSNVSVYRTOHTGVLKIVTLWAVVLAFL-----VNGPMLVSESKDEGSEC- 164
Qy 199 STNEYTTLMGY--YHLLVQIPDIFFTVVVMLITTKI-----LQ 236
Db 165 -----EPGFSEYIIAITSFLEVPVILVAVFNMNIYWSLWKROHLSRCQSHPGLT 217
Qy 237 ALNIRI-GTRFSTGOKKARKKTTISLTTOHEATDMSOSSGGR-NVFGVRTSV-SVITA 293
Db 218 AVSSNICGHSF---RGLSSRRSLSASTVEPASHSRQRKSSLMFSSRTKMSNTIA 273
Qy 294 LRR-----AVKRH-RERR--RQKRVFRMSLLIISTFLLCWTPIS-----VLNITLCL 339
Db 274 SKMGFSQSQSDVALHOREHVELLRARLAKSLAILLGVFAVCWAPVSLFTIVLSFYSSAT 333
Qy 340 GPSDLLVLRCLFLVMAYGTTIFHPLLYAFTQKQKVLKSKMKRVVSVIVEADPLPN 397
Db 334 GPKS--VMYRIAFWLQWNSFV-NPLLYPLCHKRFQKAFK-----IFCIKKQPLPS 382
RESULT 10
US-10-005-010-4
; Sequence 4, Application US/10005010
; Patent No. US20020115149A1
; GENERAL INFORMATION:
; APPLICANT: Weinshank et al, Richard L.
; TITLE OF INVENTION: Method of Obtaining A Composition Comprising A 5-HT1D
; TITLE OF INVENTION: Selective Compound
; FILE REFERENCE: 36536-B4
; CURRENT APPLICATION NUMBER: US/10/005,010
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/371,705
; FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-010-4
Query Match 8.9%; Score 195; DB 12; Length 390;
Best Local Similarity 19.5%; Pred. No. 2.3e-10;
Matches 78; Conservative 90; Mismatches 175; Indels 58; Gaps 14;
Qy 5 PILETNMSESITVRDIDDDINTWYQPLSPFQSVLSTGFL-MLEIVLGLGNLTVL 63
Db 21 POANLESAPSONCSARDY-----YQD-SISLPKVLVLLALITLITLSNAFVIA 72
Qy 64 VLYCKSNLINSVSNITLNLHVLVDVIVCGICPILVILLLESNTALICCFHEACVS 123
Db 73 TVI---RTRKLHPTANLIASLAVTOLLVILVMPISTMTVTVGRWTLGVQVCDWLSSDI 130
Qy 124 FASVSTAINVFAITLDRY-----DISVKPANRILTMGRVAVLMISWIFSFSLIPFIEV 179
Db 131 TCTTASILHLVIALDRYWAITDAVEYSKR--TPKRAVMIALVWVFSISISLPPFF-- 186
Qy 180 NFPSLQSGNTW-----ENKTLICVSTNEYTELGYHLLVQIPDIFFTVVVMLITY---- 231
Db 187 -----WRQAAEEVSECVNYTDH-----ILYTVYSTVGAFYFPFTLLILYGR 231
Qy 232 -----TKILQALNIRIGTRFSTGOKKARKKTTISLT--OHEATDMSOSSGGRNVFVGR 285
Db 232 YVEARSRLIKQTPNRTGKRLTRAQLITDPSGTSSTSVTSINSRVPDVPSESGSPVTVNQVK 291

Qy 286 TSVSVIIARRAVKRHRERERQKRVFRMSLLIISTFLLCWTPISVNLNTTI-LICGPSDL 344
Db 292 VYSDALLEKKLMAAR-----KATKTLGITLGAIVCWLPFFFIISLVMPICKDACWF 346
Qy 345 LVKRLCLFLVMAYGTTIFHPLLYAFT-----RQKQKVLASK 381
Db 347 HLAIFDFFTWGLYNSLINPIIYITMSNEDFKQAFHKLIREK 387
RESULT 11
US-08-681-219-31
; Sequence 31, Application US/08681219
; Patent No. US20020058607A1
; GENERAL INFORMATION:
; APPLICANT: Takaaki Sato and Junn Yanagisawa
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
; TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,219
; FILING DATE: 22-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 481 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-681-219-31
Query Match 8.9%; Score 195; DB 8; Length 481;
Best Local Similarity 20.8%; Pred. No. 3e-10;
Matches 90; Conservative 83; Mismatches 167; Indels 92; Gaps 19;
Qy 48 LMLEIVLGLGSLTVLVLVLCMKSNLINSVSNITLNLHVLVDVIVCGICPILFTVILLSL 107
Db 61 ILMWIPTTGGNTVLIVALSLEKLL-QYAFNFMLSLAVADLLVGLFVMPIALLTIMFEA 119
Qy 108 ESNTALIC-----FHBACVSFASVSTAINVFAITLDRYDISVKP--ANRILTMGRVAVLM 161
Db 120 MWPLPLVLCPAWFLDLVLFSTASI---MHLCAISVDRIATAIKKPIQAOVNSRATAFIKI 176
Qy 162 ISIWTFSPFSLIPFIEVNFSSQSGNTWENKTLICVSTNEYTELGYHLLVQIPDIF 221
Db 177 TVVWLIS-IGIAP-VPIKGIETVDNP---NNITCVLTKERFGD-----FMLFGSLAARF 227
Qy 222 FTWVWMLIYTILOALNIRIGTRFSTGOKKARKK-----TISLTTOHEATDMS 272
Db 228 TPLAINIVTYFTLHAL-----QKKAYLVKNKPPQRLTWLTVTSTVFQDETSPCS 276
Qy 273 Q-----SSGGRNVFVGRVTSVSVIILARRAVKRHRERERQKRVFRMS 315

Db 336 FCDPSRDDYETIAMSTMHTDVSKTSLKQASPV-----AFKKISMNDNE 380

RESULT 7

US-09-885-478-4

Sequence 4, Application US/09885478

Patent No. US20020111306A1

GENERAL INFORMATION:

APPLICANT: SALON, JOHN A

APPLICANT: LAZ, THOMAS M

APPLICANT: NAGORNY, RAISA

APPLICANT: WILSON, AMY E

TITLE OF INVENTION: DNA ENCODING A HUMAN MELANIN CONCENTRATING HORMONE RECEPTOR (MCH)

TITLE OF INVENTION: US985-478

FILE REFERENCE: 1795/57453-A-PCT-US

CURRENT APPLICATION NUMBER: US/09885,478

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: PCT/US99/31169

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 353

TYPE: PRT

ORGANISM: RATTUS NORVEGICUS

US-09-885-478-4

Query Match 9.2%; Score 201; DB 10; Length 353;

Best Local Similarity 22.5%; Pred. No. 5.7e-11;

Matches 87; Conservative 59; Mismatches 141; Indels 100; Gaps 12;

Qy 22 DIDDINTNMVQPLSYPLSFQVSLTGFLMLEI-----VLGLSNTLVLYCMKSNL--IN 74

Db 16 NISGDQDNLTPGSPPTGVSVINIIMPVFGTICLLGIYGNSTVIFAVVKKSLHWCS 75

Qy 75 SVSNIITMNLHVLVDIVCGIPL-----TVILLLESNTALICCFHE 119

Db 76 NVPIFIFINLSVDLLFLG-MPMIHQLMGVWVHGETMCTILITANDANSQF----- 128

Qy 120 ACVSFASVSTAINFAITLDKYISVKP--ANRILTMGRVAMLMISWIFSFSLIPFI 177

Db 129 -----TSTVI-LTAMTIDRYLATVHPISSTKFKRPSMATVLCLLWALSFSITPW 180

Qy 178 EVNPFESQSGTWNKTLCLVSTNEYTELGMVYHLLVQIPIFFFTVVMMLTYKILQA 237

Db 181 YARLIPFGGAVGCGIRLPNDPTDLYWFTLYQFF-LAPALPF-----VVIITAAVKKILQ- 233

Qy 238 LNIIRIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIIALRRA 297

Db 234 -----RMTSSVAPASORS 246

Qy 298 VKHRRERERQKRVFRMSLLIISTFLCWTPISVLNTILCLG-PSDLLVLRCLCFVMA 356

Db 247 I-----RLRKRVRTAIAICLVFVFCWAPYVYLQTLQSLRSPTLTFVLYNAAISLG 300

Qy 357 YGTFIFHPLLYAFTRQKQVILKSKMK 383

Db 301 YANCLAPFVYVILCFETFRKLVLVSK 327

RESULT 8

US-09-910-411-2

Sequence 2, Application US/09910411

Patent No. US20020137054A1

GENERAL INFORMATION:

APPLICANT: Bergsma, Derk

APPLICANT: Fitzgerald, Laura

APPLICANT: Li, Xiatong

APPLICANT: Michalovich, David

APPLICANT: Zhu, Yuan

TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor

FILE REFERENCE: GP70655-2C1

CURRENT APPLICATION NUMBER: US/09/910,411

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: 09/693,761

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 09/497,790

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: 09/431,898

; PRIOR FILING DATE: 1999-11-02

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapien

US-09-910-411-2

Query Match 9.0%; Score 197.5; DB 10; Length 390;

Best Local Similarity 23.4%; Pred. No. 1.4e-10;

Matches 98; Conservative 78; Mismatches 159; Indels 83; Gaps 22;

Qy 25 DINTNMVQPLS--YPLSFQVSLTGFLMLEIVLGLSNTLVLYCMKSNLINSVSNITM 82

Db 3 DTNSTINLSLSTRVTLAFMFLVAF---AIMLG---NALVILAFVVDKRLRHR-SSYEFL 55

Qy 83 NLHVLVDVLCVGCIPLTIVILLLESNTALICCFHEACVSFASVSTAINFAITLDYD 142

Db 56 NLAISDFEFGVISIPLYIPHTLFEWDFGKE-ICVFMLTDTYLLCTASVYNIVLISYDRY- 113

Qy 143 ISVAPNARILTMGRAVM---LMISWIFSFSEFLIPETIEVNFSLQSGNTWENKTLCLV 198

Db 114 LSVSNVSVYRQHTGVLKIVILMVAVWLAF-----VNGPMILYSEKWDGSEC- 164

Qy 199 STNEYTELGMV--YHLLVQIPIFFFTVVMMLTYTKI-----LQ 236

Db 165 -----EPGFSEWYILAITSFLEFIPVILVAVFNNIYMSLWKRDHLSRCQSHGLT 217

Qy 237 ALNIRI-CTREFSTGQKKARKKKTISLTQHEATDMSQSGGR-NVFGVETSV-SVILIA 293

Db 218 AVSSNICGHSF---RGLSSRRSLASASTEPASHSERQKRKSLMFSSTKMNSTIA 273

Qy 294 LRR-----AVKRH-RERRE--RQKRVFRMSLLIISTFLCWTPIIS----VLNTILCL 339

Db 274 SKMGFSQSDSVALHQREHVELLRARLAKSLAILLGVFAVCWAPYSLFTIVLSYSNT 333

Qy 340 GPSDLLVLRCLCFVMAVGTTFIFHPLLYAFTRQKQVILKSKMKRVVSVIVEADPLN 397

Db 334 GPKS--VMYRIAFWLQWFNSEV-NPLLYPLCHKRPQAKFLK-----IFCIKKQPLPS 382

RESULT 9

US-10-052-193-2

Sequence 2, Application US/10052193

Patent No. US20020132755A1

GENERAL INFORMATION:

APPLICANT: Pfizer, Inc.

TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS

FILE REFERENCE: PCI0963A

CURRENT APPLICATION NUMBER: US/10/052,193

CURRENT FILING DATE: 2002-01-17

PRIOR APPLICATION NUMBER: 0101223.6

PRIOR FILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 390

TYPE: PRT

ORGANISM: Homo sapiens

US-10-052-193-2

Query Match 9.0%; Score 197.5; DB 12; Length 390;

Best Local Similarity 23.4%; Pred. No. 1.4e-10;

Matches 98; Conservative 78; Mismatches 159; Indels 83; Gaps 22;

Qy 25 DINTNMVQPLS--YPLSFQVSLTGFLMLEIVLGLSNTLVLYCMKSNLINSVSNITM 82

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; PRIOR APPLICATION NUMBER: 09/030,582
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 08/467,568
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/US94/09051
; PRIOR FILING DATE: 1994-08-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 517
; TYPE: PRT
; ORGANISM: human
US-09-951-622-10

Query Match          9.3%; Score 207.5; DB 10; Length 517;
Best Local Similarity 19.4%; Pred. No. 2.4e-11;
Matches 81; Conservative 95; Mismatches 156; Indels 85; Gaps 16;

QY 41 QVSUTGFLMLEIVLG-----LGSNLTVLVLYCMKSNLINSVSNITMNLHVLVDVLCV 93
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 39 QLDITRAISVGLVGAFLFAIVGNILVLSVACNRH--LRPTNVFIVNLAMADLLSF 96
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 94 GCIPLTVIILLSESNTALICCFHEACVSPASVSTAINVFAITLDRYDISVKPNR--- 150
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 97 TVLPFSAALEVGVWVGLGRIFCDIAWADVLCCTASILSCAISIDRY-IGVYSLSQYPT 155
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 151 ILTMGRVWMLMISWIEFSEFSLPIPIEVNFFSLQSGNTWE-----NKTLLCVSTNE--- 202
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 156 LVTRKAILALLSVWVLSVTSIGPLL-----GWKEPAPNDDKCGVTEPPFYA 204
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 203 YYTELGMYHLLVQIPIFFFTVVVVMVLTYYTKILQALNIRIGTRFSTGQKKARKKKTISL 262
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 205 LFSSILGSFYPLAVLVVYCRVYIVAKRTKNLEA-----GVMKEMSNSKELTL 253
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 263 TTQ-----HEATDMSOSSGGRNVVFGVRTSVSVIIALRAVKRHRERERQKRVFRMSLLI 318
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 254 RIHSKNPHEDTLSSTKAKGHN-----PRSSIAVKLF-----KFSREKKAAKTLGIV 299
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 319 ISTLLCWTPTSV---LNTTILCLGPSDLLVKRLCFLVMAYGTTTFHPLLYAFTROKFO 375
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 300 VGMFILWLPFIALPLGSLSTLKPDAVKV---VFWLGYFNCLNPDIIPCSKSEK 356
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 376 KVL-----KSKMKKRVSIWEADPLPNNAVINHSW-----IDPKRNKKTTFEDS 419
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 357 RAFVRLGCQCQRGRRRR-----RRRLGGCAATYRPWTRGSLERSQSRKSLDSDS 408
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 5
US-09-771-956-2
; Sequence 2, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-956-2

Query Match          9.3%; Score 204; DB 10; Length 384;
Best Local Similarity 21.6%; Pred. No. 3.4e-11;
Matches 77; Conservative 68; Mismatches 109; Indels 102; Gaps 15;

QY 52 IVLGLSGLNLTAVLVLYCMKSNLINSVSNITMNLHVLVDVLCVPLTVIILLSS----- 106
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 50 IILGVSGNL-ALIIILKQKEMRNVNIIIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFG 108
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 107 ---LESNTALICCFHEACVSPASVSTAINVFAITL---DRVDISV-----KPNARILTMG 155
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 109 ETMCKLNPFFVQC-----VSTVTSIFSLVIAVERHQLIINPRGWRNNRHAYIG 157
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 156 RAYMLMISWIEFSEFSLPIPIEVNFFSLQSGNTWENKTLIC-----YSTNEYVTEL-CM 209
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 158 ITV-----IWLAVASSL-PEV---IYQILDEFPQVSNLAFAKDKYVCFDFPDSHRL 208
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 210 YYHLLVQIPIFFFTVVVVMVLTYYTKILQALNIRIGTRFSTGQKKARKKKTISLTQTQHEAT 269
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 209 SYTTLLLVQVYFGPLCFICYFKIY----IRLKR-----IRLKR----- 240
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 270 DMSOSSGGRNVVFGVRTSVSVIIALRAVKRHRERERQKRVFRMSLLIISTFLLCWTPI 329
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 241 -----NNMMDKIRDS-----KYRSETKRINMILLSVAVAFVAVCWLP 278
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 330 SVLNNT-----ILCLGPSDLLVKRLCFLVMAYGTTTFHPLLYAFTROKFOKVLK--- 379
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 279 TIFNTVFDNHHQIATCNHLL--FLCHLTAMISTCV-NPIFYGLNKNFORDQFFFN 335
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY 380 -----SKMKKRV---VSIEADPLPNNAVINHSWIDPKRNKKTTFEDS 420
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

```


Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	222	10.1	451	10	US-09-931-844-6		Sequence 6, Appl
2	208	9.5	384	10	US-09-962-646-15		Sequence 15, Appl
3	208	9.5	497	12	US-10-052-589-2		Sequence 2, Appl
4	207.5	9.5	517	10	US-09-951-622-10		Sequence 10, Appl
5	204	9.3	384	10	US-09-771-956-2		Sequence 2, Appl
6	203	9.3	382	10	US-09-771-956-3		Sequence 3, Appl
7	201	9.2	353	10	US-09-885-478-4		Sequence 4, Appl
8	197.5	9.0	390	10	US-09-910-411-2		Sequence 2, Appl
9	197.5	9.0	390	12	US-10-052-193-2		Sequence 2, Appl
10	195	8.9	390	12	US-10-005-010-4		Sequence 4, Appl
11	195	8.9	481	8	US-08-681-219-31		Sequence 31, Appl
12	195	8.9	481	10	US-09-919-497-72		Sequence 72, Appl
13	195	8.9	518	10	US-09-804-551B-8		Sequence 8, Appl
14	193.5	8.8	370	12	US-10-044-592-12		Sequence 12, Appl
15	193.5	8.8	370	12	US-10-044-592-74		Sequence 74, Appl
16	192.5	8.8	413	10	US-09-811-286-2		Sequence 2, Appl
17	192.5	8.8	413	10	US-09-951-622-12		Sequence 12, Appl
18	192.5	8.8	413	10	US-09-993-844-2		Sequence 2, Appl
19	192.5	8.8	413	10	US-09-990-596-1		Sequence 1, Appl

	: : : : : : : :	118	AVLCMFPTLIPNLMEFIQGEVIC---RAAYFMGLSVSVSTFNVAISERYSIAICNPL	174
Db				
	: : : : : : : : : : :	148	ANRI-LTMGRAYMLMISIWIFSFSLPIPFIEVN---FFSL-----QSGNTWENKTLL	196
QY				
	: : : : : : : : : :	175	XSRVQMTRSHAYRVIAATWVLSSI-IMPILYLVNKTVFPMKDRRVGHOCRLVWPSP	230
Db				
	: : : : : : : : : : : :	197	CYSTNEYTELGMYYHLLVQIDPFTFVVVMULTITTKILOALINIRIGTFSTGGKKKARK	256
QY				
	: : : : : : : : : : : :	231	-----QVOQAVALLLTTLTPFGVIMVAVGLISRELYRGIQFEMDLINKAEKAHK	281
Db				
	: : : : : : : : : : : :	257	KKTISLTQTQHEATD---MSQSISGGRNVVFVRTSVSVIIALLRA-VKRHRERRERQKV	311
QY				
	: : : : : : : : : : : :	282	NGVSTPTTIPSGDEGGCVIQVKRNMTMEMSTLPSTCKMDRARINSEAKLMAKRRV	341
Db				
	: : : : : : : : : : : :	312	FRMLLIISTFLCTTPISVLNT--TIILCLGPSDLLKLRLCFL-VMAYGTTTFIPLLYA	368
QY				
	: : : : : : : : : : : :	342	IRMLIVIVAMFFICMPFVANTWKAFDELSAFNTLGAPISFHLLSYTSACYNPLYIC	401
Db				
	: : : : : : : : : : : :	369	FTRQKFQKVLKMKMRKRVSVVEADPLPNNAVIHNSWDIPKRNKITPED	418
QY				
	: : : : : : : : : : : :	402	FNNKRFKFAFLGTG-----SSCIKPCNRFDOTED	431
Db				

Search completed: December 4, 2002, 16:03:12
Job time : 20 secs

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QY 197 CVSTNEYTELGMYYHLLVQIDPIFFTVVVVMLITYTKILQALNIRGTFRSTGQKKKARK 255
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 231 -----QVOQAWYVLLLTILFFIPGVVMIVAYGLISRELYRGIQFEMDLNKEAKAHK 281
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 257 KKTISLTQHEATD---MSQSSGGRNVGVGRTSVSIIALRR--VKRRRRERERQKRV 311
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 282 NGVSTPTTIPSGDEGDCYIQVTKRRNTMEMSLTTPSVCTKMDRARNINSEAKLMAKKRV 341
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 312 FRMSLLIISFLLCWTPISVINT--TTLICGSPDLLVKLRLCFL-VMAYGTTITFHPLLYA 368
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 342 IRLMIVAMFFICWPIFVANTWKAFDELSAFNTLTGAPISFIHLLSYTSACVNPILIYC 401
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 369 FTRQKPKVKLXMKMKRVSVIADPLPNNAVIHNSWIDPKRKNKKTTFED 418
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 402 FMNKRERKAFLGTF-----SSCIKPCRNFRDTDED 431
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
US-09-076-510-7
; Sequence 7, Application US/09076510
; Patent No. 6376198
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
; TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,510
; FILING DATE: 12 MAY 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/570,157
; FILING DATE: 11-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00398/109002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/428-0200
; TELEFAX: 617/438-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-076-510-7

Query Match 11.4%; Score 249.5; DB 4; Length 453;
Best Local Similarity 22.7%; Pred.No.1e-13;
Matches 93; Conservative 84; Mismatches 172; Indels 61; Gaps

QY 32 QPLSYPLSFQVSLTGLFMLEIVLGLSGNLVLYVLYCKNSLINSVNIITMNLHVLVDVII 91
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 60 KPSPSDNLNMRVIMVYGVIFLLSVFGNTLIIIVLVNKR--LRTITNSFLLSLALSOLMW 117
   :: :::: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 92 CVGCIPIITVILLLSLSNTALICCCFHEACVSPASVSTAINVF---AITLDRYDISVKP- 147

```


; GENERAL INFORMATION:
 ; APPLICANT: WANK, Stephen A.
 ; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
 ; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/029,170
 ; FILING DATE: 19930310
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/937,609
 ; FILING DATE: 02-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/928,033
 ; FILING DATE: 11-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/861,769
 ; FILING DATE: 01-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/831,248
 ; FILING DATE: 07-FEB-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 40399/166 NIHD
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 428 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-029-170-31

Query Match 11.5%; Score 253; DB 4; Length 428;
 Best Local Similarity 22.8%; Pred. No. 4.8e-14;
 Matches 95; Conservative 85; Mismatches 132; Indels 104; Gaps 18;
 Qy 15 SNITVRDIDDINTNMV-----QPLSYPLSFQVSLTGFLMLEIVGLGNS 59
 Db 12 SNITPPCELGENETFLCDDQPRPSKEWQPAVQILLYSLIFLLSV-----LGNT 60
 Qy 60 LTVLVLYCMKSNLNSVNIITMNLHLDVVICGCIPLTIVILLLESNTALICCFHE 119
 Db 61 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLFCMPFNIPNLKDFIFGSAVC---K 115
 Qy 120 ACVSFASVSTAINVP---AITLDYRDISVKP-ANRI-ITMGRVLMISWIFSF----- 169
 Db 116 TTTVMGTGSVSTFNFLVAISLERYGAICKPLQSRVWOTKSHALKVIAATWCLSFMTIP 175
 Qy 170 ---FSFLPFPEVNFPSLQSGNTWENKTL-LC--VSTNEYYTELGMYHLLVQIPFFET 223
 Db 176 YPIYSLNVPPFKNN-----NQFANMCRFLPNQV---MQQSWHTFLLLLIFLIP 221
 Qy 224 VVVMILITVKIQLALNIRIGTRFSTGQKKARKKKTISLTT-QHEATD----- 270
 Db 222 GIVMNVAYGLI--SLELYQGIKFEASQKSAKERKPSITSSGKYEDSDGCVYLQKTRPRK 279

Qy 271 -----MSQSSGGRNVVFGVRTSVSVIIARRAVKRRERERQKRVFRMSLLIISTFLLC 325
 Db 280 LELRLQSTGSSSRANRIRNSAANLMA-----KKRVIRMLIIVIVVLFLLC 325
 Qy 326 WTPISVLNTTILCLGSPDLLVKRLC-----FLVMAYGTTTFHPLLYAFTQKFO 375
 Db 326 WMPIFSANA---WRAYDTASAERRLSGTPISEFILLLSYSSCVNFIICFMKNKRR 378
 RESULT 13
 US-09-076-510-5
 ; Sequence 5, Application US/09076510
 ; Patent No. 6376198
 ; GENERAL INFORMATION:
 ; APPLICANT: Kopin, Alan S.
 ; APPLICANT: Beinborn, Martin
 ; TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
 ; TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Clark & Elbing LLP
 ; STREET: 176 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: FastSeq version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/076,510
 ; FILING DATE: 12 MAY 1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/570,157
 ; FILING DATE: 11-DEC-1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00398/109002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/428-0200
 ; TELEFAX: 617/438-7045
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 428 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-076-510-5

Query Match 11.5%; Score 253; DB 4; Length 428;
 Best Local Similarity 22.8%; Pred. No. 4.8e-14;
 Matches 95; Conservative 85; Mismatches 132; Indels 104; Gaps 18;
 Qy 15 SNITVRDIDDINTNMV-----QPLSYPLSFQVSLTGFLMLEIVGLGNS 59
 Db 12 SNITPPCELGENETFLCDDQPRPSKEWQPAVQILLYSLIFLLSV-----LGNT 60
 Qy 60 LTVLVLYCMKSNLNSVNIITMNLHLDVVICGCIPLTIVILLLESNTALICCFHE 119
 Db 61 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLFCMPFNIPNLKDFIFGSAVC---K 115
 Qy 120 ACVSFASVSTAINVP---AITLDYRDISVKP-ANRI-ITMGRVLMISWIFSF----- 169
 Db 116 TTTVMGTGSVSTFNFLVAISLERYGAICKPLQSRVWOTKSHALKVIAATWCLSFMTIP 175
 Qy 170 ---FSFLPFPEVNFPSLQSGNTWENKTL-LC--VSTNEYYTELGMYHLLVQIPFFET 223

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,510
; FILING DATE: 12 MAY 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/570,157
; FILING DATE: 11-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00398/109002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/428-0200
; TELEFAX: 617/438-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-076-510-6

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Query Match 11.7%; Score 257; DB 4; Length 443;
Best Local Similarity 23.6%; Pred. No. 2.3e-14;
Matches 102; Conservative 84; Mismatches 131; Indels 112; Gaps 21;

QY 6 ILKINMQSESNITVRDDIDININMY-----QP-LSYPLSFQVSLTGFLMLEIVLGLSN 59
DB 18 VVDSLLMNSNITPPCELGLENETLFCLOQPQPSKEWQALQILLYSIIFLSVLGNTLV 77
QY 60 LTVLVLYCMKSNILNSVNIITMNLHVLVDVVICVGCIPITIVILLLSLESNTALICCFHE 119
DB 78 ITVLI-----RNKRMRTVTNIFLLSLAVSDLMCLF-CMPENLIPNLLKDFEFGSAVC---K 129
QY 120 ACVSFASVSTAINVF---AITLDYDISVKP-ANRI-LTMGRAVMLMISWIFSF----- 169
DB 130 TTTYFMGTSSVSTFNVAISLRYGAICRPLQSRVWQTKSHALKVIAATWCLSFMTMP 189
QY 170 ---FSLPIPIEVN-----PFSLSQSG---NTWENKTLICVSTNEYYTELGMYVHLLVQ 216
DB 190 YPIYSNLEVFETKNNQNTANMCRFLPSDAMQSQWQTFLLI----- 230
QY 217 IPIFFTVVVMITYTKILQALNIRIGTRFSTGQKKARKKK-TISLTTQHEATD----- 270
DB 231 --LFLLPGLVVMVAYGLI--SLEYQIKFDASQKSAKEKRPSTGSSTRYEDSDGCLYQ 286
QY 271 -----MSQSGGRNVFVRTSVSV--IIALRAVRKRRERQRKRVFMSL 316
DB 287 KSRPPKLELQQLSGSGSGSR-LNRIRSSSAANLIA-----KKRVIRMLI 331
QY 317 LIISTELLWCPTISVNT-----TI-----LCUGPSDLLVLRCLFLVMAYGTTIFHPLL 366
DB 332 VIVVLFLLCWPFISSANWRAVDVTSAEKHLSTPISFI-----LLSYTSSCVNPII 384
QY 367 YAFTRQKFQ 375
DB 385 YCFMNRKR 393

RESULT 11
US-08-570-157-5
; Sequence 5, Application US/08570157
; Patent No. 5750353
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin

```

```

; TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
; TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,157
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00398/109001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-157-5

Query Match 11.5%; Score 253; DB 1; Length 428;
Best Local Similarity 22.8%; Pred. No. 4.8e-14;
Matches 95; Conservative 85; Mismatches 132; Indels 104; Gaps 18;

QY 15 SNITVRDDIDININMY-----QPLSYPLSFQVSLTGFLMLEIVLGLSN 59
DB 12 SNITPPCELGLENETLFCLOQPQPSKEWQPAVQILLYSLIFLSV-----LGNT 60
QY 60 LTVLVLYCMKSNILNSVNIITMNLHVLVDVVICVGCIPITIVILLLSLESNTALICCFHE 119
DB 61 LVITVL--INRKMRTVTNIFLLSLAVSDLMCLFCMPENLIPNLLKDFEFGSAVC---K 115
QY 120 ACVSFASVSTAINVF---AITLDYDISVKP-ANRI-LTMGRAVMLMISWIFSF----- 169
DB 116 TTTYFMGTSSVSTFNVAISLRYGAICRPLQSRVWQTKSHALKVIAATWCLSFMTMP 175
QY 170 ---FSLPIPIEVNPFSLQSCNTWENKTL-LC--VSTNEYYTELGMYVHLLVQIPFFFT 223
DB 176 YPIYSNLEVPFTKN-----NOTANMCRFLPNVDV---MQQSWHTFLLILFLIP 221
QY 224 VVYMLITYTKILQALNIRIGTRFSTGQKKARKKKTISLTTQHEATD----- 270
DB 222 GIWVMVAYGLI--SLEYQIKFEASQKSAKEKRPSTTSYGKVEDSDGCLYQKTRPRK 279
QY 271 -----MSQSGGRNVFVRTSVSVIIALRAVRKRRERQRKRVFMSLIIISTFLLC 325
DB 280 LELRQLSTGSSSRANRIRSNSSAANLMA-----KKRVIRMLIVIVLWFLFLC 325
QY 326 WTPISVLNITLCLGPSDLLVLRCLC-----FLVMAYGTTIFHPLLYATROKFQ 375
DB 326 WMPIFSA---WRAVDYDTASAERRLSGTPISFILLSYTSSCVNPIIYCFMNRKR 378

RESULT 12
US-08-029-170-31
; Sequence 31, Application US/08029170
; Patent No. 6169173

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-029-170-14

Query Match 12.2%; Score 266.5; DB 4; Length 444;
Best Local Similarity 23.8%; Pred. No. 3.5e-15;
Matches 102; Conservative 85; Mismatches 131; Indels 111; Gaps 20;

Qy 6 ILEINMQSESNTVRDDDDINTNMV-----QP-LSYPLSFQVSLTGFLMLEIVLGLGNS 59
Db 18 VVDSLLMNGSNITPPCELGLENELTFCLDQPOPKSQKEMQSAQILLYSIIFLLSVLGNLT 77
Qy 60 LTVLVLYCKMKNLSVNSNIITMNLHVLVDVICVGCIPLTIVILLLSLESNTALICCPHE 119
Db 78 ITVLI-----RNKRMRTVTNIFLLSLAVSDMLCLFCMPFNLPNLLKDFIFGSAVC---K 130
Qy 120 ACVSFASVSTAINVF---AITLDYDISVKP-ANRI-LTMGRVLMISWIFSF-----169
Db 131 TTTFMGTSTVSSTFNLVAISLERYGAICRPLQSRVWQTKSHALKVIAATWCLSTFTIMP 190
Qy 170 ---FSLIPFTEVN-----FFSLQSG---NTWENKTLICVSTNEYYTELGMYHLLVQ 216
Db 191 YPIYSLNVPFTKNNQNTAMCRFLPSDAMQSQWTFLLI-----231
Qy 217 IPIFFFTVVMLIYTKILOALNIRIGTFSTGQKKARKK-TISLTQHEATD-----270
Db 232 --LFLPGIVMVVAYGLI--SLEYQGIKFDASQKSAKPKSTGSTRYEDSDGCVLQ 287
Qy 271 -----MSQSSGGRNVFGRVTSV--IIALRRVAKRHRERERQKRVFMSL 316
Db 386 YCFMKNRFR 394

RESULT 9
US-08-570-157-6
Sequence 6, Application US/08570157
Patent No. 5750353
GENERAL INFORMATION:
APPLICANT: Koplin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,157

FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/109001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 443 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-570-157-6

Query Match 11.7%; Score 257; DB 1; Length 443;
Best Local Similarity 23.8%; Pred. No. 2.3e-14;
Matches 102; Conservative 84; Mismatches 131; Indels 112; Gaps 21;

Qy 6 ILEINMQSESNTVRDDDDINTNMV-----QP-LSYPLSFQVSLTGFLMLEIVLGLGNS 59
Db 18 VVDSLLMNGSNITPPCELGLENELTFCLDQPOPKSQKEMQSAQILLYSIIFLLSVLGNLT 77
Qy 60 LTVLVLYCKMKNLSVNSNIITMNLHVLVDVICVGCIPLTIVILLLSLESNTALICCPHE 119
Db 78 ITVLI-----RNKRMRTVTNIFLLSLAVSDMLCLFCMPFNLPNLLKDFIFGSAVC---K 129
Qy 120 ACVSFASVSTAINVF---AITLDYDISVKP-ANRI-LTMGRVLMISWIFSF-----169
Db 130 TTTFMGTSTVSSTFNLVAISLERYGAICRPLQSRVWQTKSHALKVIAATWCLSTFTIMP 189
Qy 170 ---FSLIPFTEVN-----FFSLQSG---NTWENKTLICVSTNEYYTELGMYHLLVQ 216
Db 190 YPIYSLNVPFTKNNQNTAMCRFLPSDAMQSQWTFLLI-----230
Qy 217 IPIFFFTVVMLIYTKILOALNIRIGTFSTGQKKARKK-TISLTQHEATD-----270
Db 231 --LFLPGIVMVVAYGLI--SLEYQGIKFDASQKSAKPKSTGSTRYEDSDGCVLQ 286
Qy 271 -----MSQSSGGRNVFGRVTSV--IIALRRVAKRHRERERQKRVFMSL 316
Db 287 KSRPPRKLQQLSGSGGSR-LNRRSSSAANLIA-----KKRVIRMLI 331
Qy 317 LIISTFLCWTPTISVLNT-----TI-----LCLGPSDLLVKRLCFLVMAYGTTIFHPLL 366
Db 332 VIVVFLCWPPIFSANAWRAYDVSAEKHLSGTPISFI-----LLSYTSSCVNPDI 384
Qy 367 YAFTRQRFQ 375
Db 385 YCFMKNRFR 393

RESULT 10
US-09-076-510-6
Sequence 6, Application US/09076510
Patent No. 6376198
GENERAL INFORMATION:
APPLICANT: Koplin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

QY 170 ---FSELPIEFIEVNFSLQSGNTWENKTLCC--VSTNEYYTELGMYYHLLVQIPIFFFTV 224
Db 196 YPIYSNLVPFTKNN---NOTGN-----MCRFLPLNDVMQOT--WHFTFLLLILFLIPG 242
QY 225 VVMILTYIKILQALNIRICTRESTGOKKARKKKTIS-----LTTQH--- 266
Db 243 IVMWAYGLI--SLEYQIKIDAIQKSAKERTKSTGSGPMWSDGCVLQKSRHPRKL 300
QY 267 EATDMSSQSGGRNVFVRTSVIIALRRVAKRHREREROKRVFRMSLLIISTFLLCW 326
Db 301 ELRQLSPSSGSRNIRIRSSSTANLMAK-----KRVIRMLIVIVLWFLFLCW 348
QY 327 TPISVLNT-----TI-----LCLGPSDLLVKLCLFVLMAYGTTIFHPLLYAFTRQKFQ 375
Db 349 MPFSANAWRAYDTVSAERHLSGTPISFI-----LLLSYTSVCVNPITYCFMKNRFR 400

RESULT 7
US-07-937-609-14
; Sequence 14, Application US/07937609
; Patent No. 5319073
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/937,609
; FILING DATE: 19920902
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,248
; FILING DATE: 07-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/861,769
; FILING DATE: 01-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,033
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/166 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-937-609-14

Query Match 12.2%; Score 266.5; DB 1; Length 444;
Best Local Similarity 23.8%; Pred. No. 3.5e-15;
Matches 102; Conservative 85; Mismatches 131; Indels 111; Gaps 20;
QY 6 ILEINMQSESNTVRDDIDINTNMY-----OP-LSYPLSFQVSLTGFLMLLEIVLGLGSN 59

Db 18 VDSLMMGNSNITPPCELGLENETIECLDQPOPSKEWQALQILLYSIIFLLSVLGNLTV 77
QY 60 LTFVLVLYCMKSNLINSVSNITMNLHVDVVICVGCIPITIVILLLSLESNTALICCFHE 119
Db 78 IIVLI---RNKEMRTVTNIFLLSLAVSDMLCLFCMPENLPNLLKDFIGSVC---K 130
QY 120 ACVSFASVSTAINVF---AITLDYDISVKP-ANRI-LTMGRAVMLMISIWIFSF----- 169
Db 131 TTTYFMGTSVSVSTFNVAISLERYGAICRPLQSRVMQTKSHALKVIAATWCLSFITMP 190
QY 170 ---FSELPIEFIEVNF-----FSLQSG---NTEWNTLLCVSTNEYYTELGMYYHLLVQ 216
Db 191 YPIYSNLVPFTKNNQNTANMCRFLPLSDAMQSQWQTFLLI----- 231
QY 217 IPIFFFTVVVMILTYIKILQALNIRICTRESTGOKKARKKKTISLTQTHEATD----- 270
Db 232 --LFLPLGVIMVAYGLI--SLEYQIKIDAIQKSAKERTKSTGSGTRYEDSDGCVLQ 287
QY 271 -----MSQSSGGRNVFVRTSVV--IIALRRVAKRHREREROKRVFRMSL 316
Db 288 KSRPPRKLEQLQSLSGSGSR-LNIRSSSSAANLIA-----KRVIRMLI 332
QY 317 LIISTFLLCWTPISVLNT-----TI-----LCLGPSDLLVKLCLFVLMAYGTTIFHPL 366
Db 333 VIVVLFCLCMPIFSANAWRAYDTVSAERHLSGTPISFI-----LLLSYTSVCVNP 385
QY 367 YAFTRQKFQ 375
Db 386 YCFMKNRFR 394

RESULT 8
US-08-029-170-14
; Sequence 14, Application US/08029170
; Patent No. 6169173
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,170
; FILING DATE: 19930310
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,609
; FILING DATE: 02-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,033
; FILING DATE: 11-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/861,769
; FILING DATE: 01-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,248
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/166 NIHD


```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0377 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 544724
US-08-919-624-3

Query Match      12.9%; Score 282; DB 2; Length 430;
Best Local Similarity 24.1%; Pred. No. 1.6e-16;
Matches 101; Conservative 83; Mismatches 127; Indels 108; Gaps 19;

QY 15 SNITVRDDDDIDNNY-----QPLSYPLSFQVSLTGLFMLEIVLGLGNS 59
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
12 SNITSACELGFENETLFCILDRPRPSKEMQPAVQILLYSLIFLSV-----LGNT 60
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 60 LVLVLYCKMKNLSNVIITMNLHVDIICVGCIPITIVILLLSLESNTALICCFHE 119
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
61 LVTIVL--IRNRMRTVTNIFLLSLAVSOLMCLFCMPFNLPISLLKDFIFGSVC--K 115
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 120 ACVSFASVSTAINVF---AITLDYDISVKP--ANRI-LTMGRAVLMIMISWIFSF----- 169
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
116 TTYFMGTSVSVSTFNVAISLERYGAICKPQSRVWQKSHALKVIAATWCLSTIMTP 175
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 170 ---FSELPIEFIEVNFSLQSGNTWENKTLIC--VSTNEYITELGMYHLLVQIPIFFTV 224
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
176 YPIYSNLVPFTKNN---NOTGN-----MCRFLLPNDVMQQT---WHTFLLLLILFLIP 222
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 225 VVMLITYTKILQALNIRIGTRFSTGOKKARKKTTIS-----LTTQH--- 266
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
223 IVMWAYGLI--SLEYQGIKFDQKSAKERKSTGSSGPMEDSDGCVLQKSRHPRKL 280
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 267 EATDMSQSGGRNVFVGVTSVSIILARRVYKRRERKRVRFRMSLLIISTFLCW 326
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
281 ELRQLSPSSSGSNRINRIRSSSTANLMAK-----KRVIRMLIVIVVLFELCW 328
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 327 TPISVLNT-----TI-----LCIGPSDLLVKRLCLFLVMAYGTTIFHPLLYAFTROKQF 375
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
329 MPIFSANAWRAYDVTSAERHLSGTPISFI-----LLLSYTSNCVNPPIYCFMKNRFR 380
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 5
US-08-029-170-23
; Sequence 23, Application US/08029170
; Patent No. 6169173
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,170
; FILING DATE: 19930310
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,609
; FILING DATE: 02-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,033
; FILING DATE: 11-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/861,769
; FILING DATE: 01-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,248
; FILING DATE: 07-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/166 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-029-170-23

Query Match      12.9%; Score 282; DB 4; Length 430;
Best Local Similarity 24.1%; Pred. No. 1.6e-16;
Matches 101; Conservative 83; Mismatches 127; Indels 108; Gaps 19;

QY 15 SNITVRDDDDIDNNY-----QPLSYPLSFQVSLTGLFMLEIVLGLGNS 59
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
12 SNITSACELGFENETLFCILDRPRPSKEMQPAVQILLYSLIFLSV-----LGNT 60
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 60 LVLVLYCKMKNLSNVIITMNLHVDIICVGCIPITIVILLLSLESNTALICCFHE 119
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
61 LVTIVL--IRNRMRTVTNIFLLSLAVSOLMCLFCMPFNLPISLLKDFIFGSVC--K 115
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 120 ACVSFASVSTAINVF---AITLDYDISVKP--ANRI-LTMGRAVLMIMISWIFSF----- 169
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
116 TTYFMGTSVSVSTFNVAISLERYGAICKPQSRVWQKSHALKVIAATWCLSTIMTP 175
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 170 ---FSELPIEFIEVNFSLQSGNTWENKTLIC--VSTNEYITELGMYHLLVQIPIFFTV 224
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
176 YPIYSNLVPFTKNN---NOTGN-----MCRFLLPNDVMQQT---WHTFLLLLILFLIP 222
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 225 VVMLITYTKILQALNIRIGTRFSTGOKKARKKTTIS-----LTTQH--- 266
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
223 IVMWAYGLI--SLEYQGIKFDQKSAKERKSTGSSGPMEDSDGCVLQKSRHPRKL 280
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 267 EATDMSQSGGRNVFVGVTSVSIILARRVYKRRERKRVRFRMSLLIISTFLCW 326
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
281 ELRQLSPSSSGSNRINRIRSSSTANLMAK-----KRVIRMLIVIVVLFELCW 328
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

QY 327 TPISVLNT-----TI-----LCIGPSDLLVKRLCLFLVMAYGTTIFHPLLYAFTROKQF 375
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
329 MPIFSANAWRAYDVTSAERHLSGTPISFI-----LLLSYTSNCVNPPIYCFMKNRFR 380
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 5
US-07-937-609-24
; Sequence 24, Application US/07937609
; Patent No. 5319073
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
```

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Matches 429; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MCFSPLEINQSSNTVRDIDINNMYPQLSPYLSFQVSLTGFLMLEIVLGLASN 60
Db 1 MCFSPLEINQSSNTVRDIDINNMYPQLSPYLSFQVSLTGFLMLEIVLGLASN 60
Qy 61 TVLVYCKMKNLSVNIITMNLHVLDVIVICVCIPLTIVILLLESNTALICCPHEA 120
Db 61 TVLVYCKMKNLSVNIITMNLHVLDVIVICVCIPLTIVILLLESNTALICCPHEA 120
Qy 121 CVSFASVSTAINVFAITLDRYDISVKPANRILTMGRAVLMISIWIFSFLLPIFEVN 180
Db 121 CVSFASVSTAINVFAITLDRYDISVKPANRILTMGRAVLMISIWIFSFLLPIFEVN 180
Qy 181 FFSQSGNTWENKILLCVSTNEYTELGMVYHLLVQIPIFFTVVMLITVKILQALNI 240
Db 181 FFSQSGNTWENKILLCVSTNEYTELGMVYHLLVQIPIFFTVVMLITVKILQALNI 240
Qy 241 RIGTRFSTGQKKKARKKKTISLTTOHEATDMSSQSGGRNVVGVRTSVSVIIALRRVAKR 300
Db 241 RIGTRFSTGQKKKARKKKTISLTTOHEATDMSSQSGGRNVVGVRTSVSVIIALRRVAKR 300
Qy 301 HRERRERKRVFRMSLLIISTFLLCWTPIISVLTNTILCLGSDLLVLRCLFLVMAYGTT 360
Db 301 HRERRERKRVFRMSLLIISTFLLCWTPIISVLTNTILCLGSDLLVLRCLFLVMAYGTT 360
Qy 361 IFHPLLAFTRQKQKVLKSKMKRVSVISVEADPLPNNAVIHNWIDPKRNNKITFEDSE 420
Db 361 IFHPLLAFTRQKQKVLKSKMKRVSVISVEADPLPNNAVIHNWIDPKRNNKITFEDSE 420
Qy 421 IREKRLVPQVYTD 433
Db 421 IREKRLVPQVYTD 433

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RESULT 2

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US-07-937-609-23
; Sequence 23, Application US/07937609
; Patent No. 5319073
; GENERAL INFORMATION:
; APPLICANT: WANK, Stephen A.
; TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
; TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/937,609
; FILING DATE: 19920902
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,248
; FILING DATE: 07-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/861,769
; FILING DATE: 01-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/928,033
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/166 NIHD

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-937-609-23

Query Match 12.9%; Score 282; DB 1; Length 430;
Best Local Similarity 24.1%; Pred. No. 1.6e-16;
Matches 101; Conservative 83; Mismatches 127; Indels 108; Gaps 19;

Qy 15 SNIVRDRDIDINNMV-----QPLSYPLSFQVSLTGFLMLEIVLGLASN 59
Db 12 SNITSACELGFENETLFCLDPRPSKEWQPAVQILLYSLIFLSV-----LGNT 60
Qy 60 LTVLVYCKMKNLSVNIITMNLHVLDVIVICVCIPLTIVILLLESNTALICCPHE 119
Db 61 LVITVL--IRNKRMTVTNIEFLSLAVSDMLCLFCMPFNLPISLLKDFIFGSVC---K 115
Qy 120 ACVSFASVSTAINVF---AITLDRYDISVKP--ANRI-LTMGRAVLMISIWIFSF----- 169
Db 116 TTTVTGTSVSVFNLVAISLRYGATCKPLQSRVMTKSHALKVIAATWCLSFITMTP 175
Qy 170 ---ESFLPIFTEVAFPSQSGNTWENKTLIC--VSTNEYTELGMVYHLLVQIPIFFTV 224
Db 176 YPIYSLNVPTKNN---NOTGN-----MCRFLLPNDVMQOT---WITFLLILFLIPG 222
Qy 225 VMLITVTKILQALNIRIGTRFSTGQKKARKKKTIS-----LTTQH----- 266
Db 223 IVMMVAYGLI--SLEYQGIKFAIQKSAKERKTSTGSSGPMEDSDGCLQKSRHPRKL 280
Qy 267 EATDMSQSGGRNVVGVRTSVSVIIALRRVAKRHRERQKRVFRMSLLIISTFLLCW 326
Db 281 ELRLSPSSSGNRINRIRSSSTANLMAK-----KRVIRMLIVIVVLFLLCW 328
Qy 327 TPISVLNT-----TI-----LCLGPSDLLVLRCLFLVMAYGTTIFHPLLAFTRQKFO 375
Db 329 MPISANAWRAYDIVSAERHLSGTPISFI-----LLSTYSSCVNPIIIFCNKRFR 380

RESULT 3
US-08-919-624-3
; Sequence 3, Application US/08919624
; Patent No. 5994097
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,624
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 16:00:33 ; Search time 18 Seconds
(without alignments)
707.785 Million cell updates/sec

Title: US-09-845-721-2

Perfect score: 2192
Sequence: 1 MCFSPLEINMQSSNITVR.....ITFEDSEIRKRLVQVWTD 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2168	98.9	433	2	US-08-919-624-1
2	282	12.9	430	1	US-07-937-609-23
3	282	12.9	430	2	US-08-919-624-3
4	282	12.9	430	4	US-08-029-170-23
5	282	12.9	450	1	US-07-937-609-24
6	282	12.9	450	1	US-08-029-170-24
7	266.5	12.2	444	1	US-07-937-609-14
8	266.5	12.2	444	1	US-08-029-170-14
9	257	11.7	443	1	US-08-570-157-6
10	257	11.7	443	4	US-09-076-510-6
11	253	11.5	428	1	US-08-570-157-5
12	253	11.5	428	4	US-08-029-170-31
13	253	11.5	428	4	US-09-076-510-5
14	249.5	11.4	453	1	US-08-570-157-7
15	249.5	11.4	453	4	US-09-076-510-7
16	240.5	11.0	449	1	US-08-570-157-1
17	240.5	11.0	449	4	US-08-570-157-2
18	239	10.9	371	1	US-08-415-818-6
19	239	10.9	371	2	US-08-894-236-6
20	239	10.9	371	2	US-08-919-624-4
21	239	10.9	371	5	PCT-US96-01444-6
22	223	10.2	451	1	US-08-570-157-2
23	223	10.2	451	4	US-09-076-510-2
24	222.5	10.2	452	1	US-07-937-609-16
25	222.5	10.2	452	4	US-08-029-170-16
26	222	10.1	422	1	US-07-817-920-3
27	222	10.1	422	1	US-08-370-542-3

Query Match 98.9% ; Score 2168 ; DB 2 ; Length 433 ;
Best Local Similarity 99.1% ; Pred. No. 1.2e-177 ;

28	222	10.1	422	1	US-08-117-006-3	Sequence 3, Appl1
29	222	10.1	422	1	US-08-216-594-3	Sequence 3, Appl1
30	222	10.1	422	1	US-08-542-358-3	Sequence 3, Appl1
31	222	10.1	422	2	US-08-157-185-13	Sequence 13, Appl
32	222	10.1	422	2	US-08-281-526B-13	Sequence 13, Appl
33	222	10.1	422	3	US-09-018-351-3	Sequence 3, Appl1
34	222	10.1	422	4	US-09-332-837-13	Sequence 13, Appl
35	222	10.1	422	5	PCT-US93-00149-3	Sequence 3, Appl1
36	219.5	10.0	411	3	US-08-817-869-3	Sequence 3, Appl1
37	219.5	10.0	411	5	PCT-US95-14377-3	Sequence 3, Appl1
38	219	10.0	447	1	US-07-937-609-29	Sequence 29, Appl
39	219	10.0	447	4	US-08-029-170-29	Sequence 29, Appl
40	218	9.9	447	1	US-07-978-892A-6	Sequence 6, Appl1
41	217.5	9.9	448	4	US-08-570-157-3	Sequence 3, Appl1
42	217.5	9.9	448	4	US-09-076-510-3	Sequence 3, Appl1
43	217	9.9	513	2	US-08-406-855A-21	Sequence 21, Appl
44	217	9.9	513	3	US-09-206-898-21	Sequence 21, Appl
45	214	9.8	453	1	US-07-937-609-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-919-624-1
; Sequence 1, Application US/08919624
; Patent No. 5994097
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,624
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0377 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CARDNOT01
; CLONE: 282414
US-08-919-624-1

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XX 08-AUG-1996..
XX
XX 30-JAN-1996; 96WO-US01444.
XX
XX 03-APR-1995; 95US-0415818.
XX 03-FEB-1995; 95US-0383746.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Cascleri MA, Linemeyer DL, MacNeil DJ, Shiao L;
XX Strader C, Tan CP, Weinberg DH;
XX
XX WPI; 1996-371369/37.
XX N-PSDB; AAT36127.
XX
XX DNA mol. encoding neuro:peptide Y Yx receptor - useful in assays to
XX identify cpds which bind to receptor, useful to treat, e.g.
XX obesity, diabetes, cardiac vasospasm and Parkinson's disease
XX
XX Claim 38; Page 49-50; 65pp; English.
XX
XX Mouse neuropeptide Y Yx (NPY Yx) receptor (AAW02099), a novel
XX subtype of NPY, is a G-protein coupled receptor having 7
XX transmembrane-spanning domains. Its amino acid sequence was
XX deduced from a genomic DNA fragment (AAT36127) obtd. from a mouse
XX cosmid library. Vectors were constructed to allow expression of
XX the murine NPY Yx receptor in mammalian (COS-7) cells. The
XX recombinant receptor, or transformed host cells, can be used to
XX screen for cpds. that modulate the function of the receptor, or
XX modulate the expression of nucleic acids encoding the receptor.
XX Such cpds. are useful for treating a variety of disease
XX conditions.
XX
XX Sequence 371 AA;
XX
Query Match 10.9%; Score 239; DB 17; Length 371;
Best Local Similarity 23.3%; Pred. No. 1.2e-16;
Matches 90; Conservative 60; Mismatches 109; Indels 128; Gaps 17;
QY 52 IVLGSGNLTVLVLYCMKNSLINSVNIITMNLHLVDLVICVCIPITIVILLLS--LES 109
DB 46 LMGIFGNLSLIIIIIPKKREAOQNVNLIANLSLDILVCVMCIPTVIYTLMDHWVFG 105
QY 110 NTALICCFHEACVSFASSTAI-NVFAITLDYDISVKPANRILTMGRAVMLMISWIFS 168
DB 106 NT---MCKLTSYVQSVSVSIFSLVLIATERYQLVINPRGMPRVAHAYWGILWLIS 162
QY 169 -----FFSFLI---PF-----IEVNFSLQSG--NTWENK-TLLCVSTN----EYYTEL 207
DB 163 LTLSPFLSLYHLTNEPFFHNLSDPTDIYTHQVACVEIWPSEKLNQLLSTSLFMLQYFVPL 222
QY 208 GMYHYLLVQIPIFFTVVVMLTYYTKILQALNIRIGTRFSTGQKKKARKKKTISLTQHE 267
DB 223 GF-----ILICYLKIVLCI-----RKRT----- 240
QY 268 ATDMSQSGGNVNVFGVRTSVSVIIALRAVKRHRERER---OKRVFRMSLLIISTELL 324
DB 241 -----ROVDRKENKSNLENKRVNVMLSIVVTFGA 272
QY 325 CWTPISVLNT-----TILCLGPSDLLVKRLGFLVMAYGTTIFHPLLYAFTRQKFKVL 378
DB 273 CWLPLNIFNVFDWYHEMLMSCHHDLV--FVCHLI-AMVSTCINPLFYGFLNKNFKQDL 329
QY 379 KSKMKRVRVSIYEADLPNNAVIHNSW 405
DB 330 M-----MLIHHCW 337
```

CC anxiety or panic, withdrawal response produced by chronic cerebral or
CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cerebral palsy,
CC spinal chord and head injury, poisoning by neurotoxins, infertility,
CC adenomas, obesity or diabetes. The use of the mutant PHRs provides for
CC the more sensitive detection of PHR agonists or antagonists.
CC Note: The present sequence does not appear in the specification; it
CC has been made by modifying the wild type human CCK-A receptor
CC sequence which is provided in pages 54-55.

XX Sequence 428 AA;

Query Match 11.5%; Score 253; DB 18; Length 428;
Best Local Similarity 22.7%; Pred. No. 4.5e-18;
Matches 94; Conservative 86; Mismatches 134; Indels 100; Gaps 18;

QY 15 SNITVRDIDDINTMY-----QPLSYPLSFQVSLTGFLMLEIVGLGNS 59
DB 12 SNITPPCELGLENETLFCLDQPRPSKEQPAVQILLYSLIFLLSV-----LGNT 60
QY 60 LTVLVLYCMKNSLINSVNIITMNLHVDVLCVGCIPLTIVILLLESNTALICCFHE 119
DB 61 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLFCMPFNLPNLKDFIFGSAVC---K 115
QY 120 ACVSFASVSTAINVF---AITLDYDISVKP--ANRI-LTMGRVLMISWIFSF----- 169
DB 116 TTTYPMTGTSVSSTENLVLSLQRYGAICKPLQSRVWQTKSHALKVIAATWCLSFITWP 175
QY 170 ---FSFLPFTIEVNFSSQSGNTWENKTL-LC--VSTNEYYTELGMVYHLLVQIPFFET 223
DB 176 YPIYSNLVPFTKNN-----NOTANMCRFLPNV---MQOSWHTFLLLLFLIP 221
QY 224 VVMLITVTKILOALNIRIGTFSTGQKKARKKKTISLTT--QHEATD----- 270
DB 222 GIVMVAAYGLI--SLELYQGIKFASQKSAKERKPTSSGKYEDSDGCVLQKTRPPRK 279
QY 271 ---MSQSGGRNVFVGVTSVSVIIALRRVRREREROKRVFRMSLLIISTFLLCWT 327
DB 280 LELRLQSTGSSSRANRIRNSNSAHSAAK-----KRVIRMLIVIVVFLCWM 327
QY 328 PISVLTNTILCLGPSDLLVKRLC-----FLVMAYGTTIFHPLLYAFTROKFO 375
DB 328 PIFSANA---WRAYDTASAERRLSGTPISFILLLSYTSVCVNPPIIYCFMKNRFR 378

RESULT 14
AAB66630
ID AAB66630 standard; protein: 428 AA.

XX AAB66630;
XX
XX
XX 05-APR-2001 (first entry)
XX Human CCK A receptor protein.
XX Cholecystokinin; CCK receptor; purify.

XX Homo sapiens.

XX US6169173-B1.

XX 02-JAN-2001.

XX 10-MAR-1993; 93US-0029170.

XX 07-FEB-1992; 92US-0831248.

XX 01-APR-1992; 92US-0861769.

XX 11-AUG-1992; 92US-0928033.

XX 02-SEP-1992; 92US-0937609.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wank SA;

XX

WPI; 2001-136725/14.

XX New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for
XX producing and purifying human CCK receptor protein to
XX sequenceable-grade homogeneity -

XX Disclosure; Fig 13; 82pp; English.

XX The present invention relates to a cholecystokinin (CCK) receptor
XX protein. The CCK receptor-encoding DNA molecule is useful for
XX expressing and purifying CCK receptor protein to
XX sequenceable-grade homogeneity. The CCK receptor proteins
XX or fragments are useful for obtaining antibodies that can
XX recognize CCK-expressing cells. The transformed eukaryotic cell
XX lines are useful for studying the receptor in an environment
XX similar to its native environment, e.g. in the context of
XX studying the electrophysiology or binding properties of the receptor.
XX The transformed prokaryotic or insect cell line is useful for
XX expressing CCK receptor to produce large amounts of the receptor for
XX immunological purposes or for studying protein structure, e.g.
XX crystallography.

XX Sequence 428 AA;

Query Match 11.5%; Score 253; DB 22; Length 428;
Best Local Similarity 22.8%; Pred. No. 4.5e-18;
Matches 95; Conservative 85; Mismatches 132; Indels 104; Gaps 18;

QY 15 SNITVRDIDDINTMY-----QPLSYPLSFQVSLTGFLMLEIVGLGNS 59
DB 12 SNITPPCELGLENETLFCLDQPRPSKEQPAVQILLYSLIFLLSV-----LGNT 60
QY 60 LTVLVLYCMKNSLINSVNIITMNLHVDVLCVGCIPLTIVILLLESNTALICCFHE 119
DB 61 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLFCMPFNLPNLKDFIFGSAVC---K 115
QY 120 ACVSFASVSTAINVF---AITLDYDISVKP--ANRI-LTMGRVLMISWIFSF----- 169
DB 116 TTTYPMTGTSVSSTENLVLSLQRYGAICKPLQSRVWQTKSHALKVIAATWCLSFITWP 175
QY 170 ---FSFLPFTIEVNFSSQSGNTWENKTL-LC--VSTNEYYTELGMVYHLLVQIPFFET 223
DB 176 YPIYSNLVPFTKNN-----NOTANMCRFLPNV---MQOSWHTFLLLLFLIP 221
QY 224 VVMLITVTKILOALNIRIGTFSTGQKKARKKKTISLTT--QHEATD----- 270
DB 222 GIVMVAAYGLI--SLELYQGIKFASQKSAKERKPTSSGKYEDSDGCVLQKTRPPRK 279
QY 271 ---MSQSGGRNVFVGVTSVSVIIALRRVRREREROKRVFRMSLLIISTFLLC 325
DB 280 LELRLQSTGSSSRANRIRNSNSAANLMA-----KRVIRMLIVIVVFLFLC 325
QY 326 WTPISVLTNTILCLGPSDLLVKRLC-----FLVMAYGTTIFHPLLYAFTROKFO 375
DB 326 WMPIFSANA---WRAYDTASAERRLSGTPISFILLLSYTSVCVNPPIIYCFMKNRFR 378

RESULT 15

AAW02099

ID AAW02099 standard; Protein: 371 AA.

XX AAW02099;

XX 25-OCT-1996 (first entry)

XX Mouse neuropeptide Y Yx receptor.

XX Neuropeptide Y Yx receptor; NPY Yx; G-protein coupled receptor;

XX obesity; diabetes; cardiac vasospasm; Parkinson's disease.

XX Mus sp.

XX WO9623809-A1.

XX

```
PD 19-JUN-1997.
XX 11-DEC-1996; 96WO-US19958.
XX 03-SEP-1996; 96US-0718047.
PR 11-DEC-1995; 95US-0570157.
XX (NEWB-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
PA Beinborn M, Kopin AS;
XX WPI; 1997-332726/30.
XX Assay for peptide hormone receptor ligand using mutant forms of the
PT receptors - where changes in second messenger signalling activity
PT indicate that a compound is an agonist
XX Disclosure; Pages 54-55; 88pp; English.
XX This is the human peptide hormone cholecystokinin (hCCK) receptor A.
CC A mutant form of this receptor can be created by substitution of certain
CC aminoacids (AAW29104). The mutant form of this receptor can be used in a
CC a novel method for determining whether a candidate compound is an
CC agonist or an antagonist of a peptide hormone receptor (PHR). The
CC candidate compound is exposed to the mutant form of the PHR that has the
CC ability to amplify the activity of an agonist as compared to the
CC corresponding wild-type receptor. A change in the second messenger
CC signalling activity of the enhanced receptor can be measured to indicate
CC whether the candidate compound is an agonist or an antagonist. The
CC agonists and antagonists can be used for treating or preventing the
CC disorders involving PHRs. They can be used for treating tumours,
CC gastrointestinal disorders, central nervous system disorders, neuroleptic
CC systems, anxiety or panic, withdrawal disorders of appetite regulatory
CC treatment or abuse of drugs or alcohol, stress, stroke, hypoglycaemia,
CC cerebral palsy, spinal chord or alcohol, stress, stroke, hypoglycaemia,
CC infertility, adenomas, obesity or diabetes. The use of the mutant PHRs
CC provides for the more sensitive detection of PHR agonists or
CC antagonists.
XX SQ Sequence 428 AA;
Query Match 11.5%; Score 253; DB 18; Length 428;
Best Local Similarity 22.8%; Pred. No. 4.5e-18;
Matches 95; Conservative 85; Mismatches 132; Indels 104; Gaps 18;
QY 15 SNTTVRDDIDDINTNMY-----OPLSVPLSFQVSLGFLMLVLVLGSGN 59
DB 12 SNTTPCELEGETNETLFCLDQPRPSKEWQPAVQILLYSLIFLSV-----LGNT 60
QY 60 LTVLVLYCMKSNLINSVNIITMNLHVLVDVLCVGCIPLTIVILLLSLENTALICCFHE 119
DB 61 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLFCMPENLIPNLKDFIGSAVC--K 115
QY 120 ACVSFASVSTAINVF--AITLDYDISVKP-ANRI-LTMGRAVMLMISWIFSF----- 169
DB 116 TTYTFMGTSVSVTFNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFITMP 175
QY 170 ---FSFLPIEYVNFESLQSGNTWENKTL-LC--VSTNEYTYELGMYYHLLVOIPFFFT 223
DB 176 YPIYSNLVPTKNN-----NOTANMCRFLPNQV---MQQSHFTLLLLILFLIP 221
QY 224 VVYMLITYTKILQALNIRIGTRFSTQKKKARKKTKISLTT-QHEATD----- 270
DB 222 GIVMWAYGLI--SLEYQIKFEASQKSAKPKFTTSSGKYEDSDGCGYLQKTRPPK 279
QY 271 -----MSQSGGRNVFVGTSVTSVIALBRAVRRERKRVRMSLLIISTFLLC 325
DB 280 LELRLQSLTGSSSRANRIRNSSAANLMA-----KKRVIRMLIVTWLFFLC 325
QY 326 WTPISVNLNTTILCGSPDLLVKLRIC-----FLVMAYGTTIFHPLLXYAFTROKQ 375
DB 326 WMPIFSANA---WRAYDTASAEERLSGTPISFILLYSYSSCVNPIIYCFMNRKR 378
```

RESULT 13
AAW29104

ID AAW29104 standard; protein; 428 AA.

XX AAW29104;

XX 12-FEB-1998 (first entry)

XX Enhanced CCK-A/gastrin receptor MH21/35.

XX cholecystokinin; CCK; peptide hormone receptor; PHR; neuropeptide;
XX mutant; messenger signal; agonist; antagonist; human; treatment;
XX tumour; gastrointestinal disorder; central nervous system disorder;
XX neurotoxin; substitution; enhanced receptor; hypoglycaemia, MH21/35.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 138 /label= E1380

FT /note= "wild type Glu is replaced by Gln"

FT Misc-difference 303 /label= A303H

FT /note= "wild type Ala is replaced by His"

FT Misc-difference 304 /label= N304V

FT /note= "wild type Asn is replaced by Val"

FT Misc-difference 305 /label= L305S

FT /note= "wild type Leu is replaced by Ser"

FT Misc-difference 306 /label= M306A

FT /note= "wild type Met is replaced by Ala"

XX W09721731-A1.

PN 19-JUN-1997.

XX 11-DEC-1996; 96WO-US19958.

XX 03-SEP-1996; 96US-0718047.

PR 11-DEC-1995; 95US-0570157.

XX (NEWB-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Beinborn M, Kopin AS;

XX WPI; 1997-332726/30.

XX Assay for peptide hormone receptor ligand using mutant forms of the
XX receptors - where changes in second messenger signalling activity
XX indicate that a compound is an agonist

XX Claim 34; Pages -; 88pp; English.

XX This mutant CCK-A receptor M21/35 is derived from the human peptide
XX hormone cholecystokinin (hCCK) receptor A. This enhanced receptor MH21/35
XX is created by the substitution of wild type Glu to Gln at amino acid
XX position 138 and wild type Ala, Asn, Leu, Met to His, Val, Ser, Ala
XX respectively at amino acid positions 303 to 306. This mutant receptor can
XX be used in a novel method for determining whether a candidate compound is
XX an agonist or an antagonist of a peptide hormone receptor (PHR). The
XX candidate compound is exposed to the mutant form of the PHR that has the
XX ability to amplify the activity of an agonist as compared to the
XX corresponding wild-type receptor. A change in the second messenger
XX signalling activity of the enhanced receptor can be measured to indicate
XX whether the candidate compound is an agonist or an antagonist. The
XX agonists and antagonists can be used for treating or preventing disorders
XX involving PHRs. They can be used for treating tumours, gastrointestinal
XX disorders, central nervous system disorders, neuroleptic disorders,
XX depression, schizophrenia, disorders of appetite regulatory systems,


```
XX CC The present invention relates to a cholecystokinin (CKK) receptor
CC protein. The CKK receptor-encoding DNA molecule is useful for
CC expressing and purifying CKK receptor protein to
CC sequenceable-grade homogeneity. The CKK receptor proteins
CC or fragments are useful for obtaining antibodies that can
CC recognize CKK-expressing cells. The transformed eukaryotic cell
CC lines are useful for studying the receptor in an environment
CC similar to its native environment, e.g. in the context of
CC studying the electrophysiology or binding properties of the receptor.
CC The transformed prokaryotic or insect cell line is useful for
CC expressing CKK receptor to produce large amounts of the receptor for
CC immunological purposes or for studying protein structure, e.g.
CC crystallography.
XX CC
XX Sequence 430 AA;
XX
XX Query Match 12.9%; Score 282; DB 22; Length 430;
XX Best Local Similarity 24.1%; Pred. No. 3.7e-21;
XX Matches 101; Conservative 83; Mismatches 127; Indels 108; Gaps 19;
XX
XX QY 15 SNITVRDDIDDINTMY-----QPLSYPLSFQVSLTGFMLLEIVLGLSN 59
XX DB 12 SNITSACELGFENETLFCIDRPPRSKEWQPAVQILLYSLIFLSV-----LGMT 60
XX
XX QY 60 LTVLVLYCKMSNLINSVNIITMNLHVDIICVGCIPLTIVILLLSLESNTALICCFHE 119
XX DB 61 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLCFMPFNLPISLLKDFIGSAVC---K 115
XX
XX QY 120 ACVSFASYSTAINVF---AITLDYDISVKP-ANRI-LTMGRAVLMISIWFSF----- 169
XX DB 116 TTTYEMGTSVSVSTNLVAISLERYGAI CKPLQSRVWQTKSHALKAVIAATWCLSTIMTP 175
XX
XX QY 170 ---FSLPIPFIEVNFPSLQSGNTWENKLLC--VSTNEYYTELGMYYHLLVQIPFFFTV 224
XX DB 176 YPIYSLNLPFTKNN---NOTGN-----MCRFLPNVDVMQQT---WHTFLLLILFLIPG 222
XX
XX QY 225 VVMLITYTKILOALNIRIGTRFSTGQKKARKKKTIS-----LTTQH--- 266
XX DB 223 IVMWAYGLI--SLEYOGIKFDAIQKSAKERKSTSGSGPMEDSDGICYLQKSRHPRKL 280
XX
XX QY 267 EATDMSQSGGRNVVFGVRTSVSVIIALRRVAKRHREROKRVFRMSLLIISTFLICW 326
XX DB 281 ELRQLSPSSSGSNRINRIRSSSTANLMAK-----KRVIMLIVIVVLFELCW 328
XX
XX QY 327 TPISVLNT-----TI-----ICLGPSDLLVLRCLFLVMAYGTTTFHPLLAFTRKQFQ 375
XX DB 329 MPIFSANAWRAYDVTVAERHLSGTPISEI-----LLLSYTSNCVNPIIYCFMKNRFR 380
XX
XX RESULT 8
XX AAB66626
XX ID AAB66626 standard; protein; 450 AA.
XX AC AAB66626;
XX DT 05-APR-2001 (first entry)
XX DE Guinea pig CKK receptor protein #2.
XX KW Cholecystokinin; CKK receptor; purify.
XX OS Cavia sp.
XX PN US6169173-B1.
XX PD 02-JAN-2001.
XX PF 10-MAR-1993; 93US-0029170.
XX PR 07-FEB-1992; 92US-0831248.
XX PR 01-APR-1992; 92US-0861769.
XX PR 11-AUG-1992; 92US-0928033.
```

```
PR 02-SEP-1992; 92US-0937609.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Wank SA;
XX WPI; 2001-136725/14.
XX New cholecystokinin (CKK) receptor-encoding DNA molecule, useful for
XX producing and purifying human CKK receptor protein to
XX sequenceable-grade homogeneity -
XX Disclosure; Fig 7; 82pp; English.
XX
XX The present invention relates to a cholecystokinin (CKK) receptor
XX protein. The CKK receptor-encoding DNA molecule is useful for
XX expressing and purifying CKK receptor protein to
XX sequenceable-grade homogeneity. The CKK receptor proteins
XX or fragments are useful for obtaining antibodies that can
XX recognize CKK-expressing cells. The transformed eukaryotic cell
XX lines are useful for studying the receptor in an environment
XX similar to its native environment, e.g. in the context of
XX studying the electrophysiology or binding properties of the receptor.
XX The transformed prokaryotic or insect cell line is useful for
XX expressing CKK receptor to produce large amounts of the receptor for
XX immunological purposes or for studying protein structure, e.g.
XX crystallography.
XX
XX Sequence 450 AA;
XX
XX Query Match 12.9%; Score 282; DB 22; Length 450;
XX Best Local Similarity 24.1%; Pred. No. 3.9e-21;
XX Matches 101; Conservative 83; Mismatches 127; Indels 108; Gaps 19;
XX
XX QY 15 SNITVRDDIDDINTMY-----QPLSYPLSFQVSLTGFMLLEIVLGLSN 59
XX DB 32 SNITSACELGFENETLFCIDRPPRSKEWQPAVQILLYSLIFLSV-----LGMT 80
XX
XX QY 60 LTVLVLYCKMSNLINSVNIITMNLHVDIICVGCIPLTIVILLLSLESNTALICCFHE 119
XX DB 81 LVITVL--IRNKRMTVTNIFLLSLAVSDMLCLCFMPFNLPISLLKDFIGSAVC---K 135
XX
XX QY 120 ACVSFASYSTAINVF---AITLDYDISVKP-ANRI-LTMGRAVLMISIWFSF----- 169
XX DB 136 TTTYEMGTSVSVSTNLVAISLERYGAI CKPLQSRVWQTKSHALKAVIAATWCLSTIMTP 195
XX
XX QY 170 ---FSLPIPFIEVNFPSLQSGNTWENKLLC--VSTNEYYTELGMYYHLLVQIPFFFTV 224
XX DB 196 YPIYSLNLPFTKNN---NOTGN-----MCRFLPNVDVMQQT---WHTFLLLILFLIPG 242
XX
XX QY 225 VVMLITYTKILOALNIRIGTRFSTGQKKARKKKTIS-----LTTQH--- 266
XX DB 243 IVMWAYGLI--SLEYOGIKFDAIQKSAKERKSTSGSGPMEDSDGICYLQKSRHPRKL 300
XX
XX QY 267 EATDMSQSGGRNVVFGVRTSVSVIIALRRVAKRHREROKRVFRMSLLIISTFLICW 326
XX DB 301 ELRQLSPSSSGSNRINRIRSSSTANLMAK-----KRVIMLIVIVVLFELCW 348
XX
XX QY 327 TPISVLNT-----TI-----ICLGPSDLLVLRCLFLVMAYGTTTFHPLLAFTRKQFQ 375
XX DB 349 MPIFSANAWRAYDVTVAERHLSGTPISEI-----LLLSYTSNCVNPIIYCFMKNRFR 400
XX
XX RESULT 9
XX AAR38890
XX ID AAR38890 standard; protein; 444 AA.
XX AC AAR38890;
XX DT 07-FEB-1994 (first entry)
XX DE Sequence encoded by the rat pancreatic cholecystokinin (CKK) A
XX receptor cDNA clone.
```

```

Db 361 IFHPLLAFTRQRFQKVLKSKMKRRVSVIYVADPLPNNVHNSWIDPKRKKITTFDSE 420
QY 421 IREKRLVPQVVT 433
    |||| |||||
Db 421 IREKCLVPQVVT 433

RESULT 6
AAR40772
XX AAR40772 standard; Protein; 430 AA.
AC AAR40772;
XX
DT 07-FEB-1994 (first entry)
XX
DE Sequence encoded by the cholecystokinin (CCK) A receptor cDNA in guinea
DE pig gallbladder and pancreas.
XX
KW Cholecystokinin receptor protein; CCK; gastrointestinal receptor.
XX
OS Cavia porcellus.
XX
FH Key
FH FT Modified-site 10
FT Location/Qualifiers
FT /label= glycosylation
FT /note= "see also AAs 12,24,190"
FT 44..67
FT /label= transmembrane domain I
FT 80..103
FT /label= II
FT 118..137
FT /label= III
FT 158..179
FT /label= IV
FT 211..234
FT /label= V
FT 316..336
FT /label= VI
FT 335..374
FT /label= VII
FT Modified-site 249
FT /label= Phosphorylation
FT /note= "see also AAs 256,274,292,300,414,416,419"
FT 411
FT /label= phosphorylation
FT
XX WO9316182-A.
XX
XX 19-AUG-1993.
XX
XX 28-JAN-1993; 93WO-US00466.
XX
XX 07-FEB-1992; 92US-0831248.
XX 01-APR-1992; 92US-0861769.
XX 11-AUG-1992; 92US-0928033.
XX 02-SEP-1992; 92US-0937609.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
XX Wank SA;
XX
XX WPI; 1993-272886/34.
XX DR N-PSDB; AAQ47669.
XX
XX Isolated DNA molecule encoding cholecystokinin receptor protein -
XX are purified to isolate cholecystokinin receptor clones and
XX produce anti-cholecystokinin receptor antibodies
XX
XX Example; Figure 6; 110pp; English.
XX
XX The rat pancreatic CCK A receptor cDNA clone encodes a protein with
XX 7 transmembrane domains, and homology with other G-protein receptor
XX superfamily members. There are 4 potential sites of N-linked

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CC glycosylation and sites for serine and threonine phosphorylation.
XX
SQ Sequence 430 AA;
Query Match 12.9%; Score 282; DB 14; Length 430;
Best Local Similarity 24.1%; Pred.No. 3.7e-21;
Matches 101; Conservative 83; Mismatches 127; Indels 108; Gaps 19;
QY 15 SNITVRDDIDDINTNMV-----OPLSYPLSFQVSLTGFMLEIVLIGLSN 59
    |||| : : : : : || : : : : : || : : : : : || : : : : :
Db 12 SNITSACELGFENETLFCDDRPRSRKQWQPAVOILLYSLIFLSV-----LGNT 60
QY 60 LTVLVLYCKMSNLINSVNIITMNLHVLVIVICVGCPIPLFIVILLLSLESNTALICCFHE 119
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LVITVL--IRNKMRTVTNIFLLSLAVSDMLCLFCMPFNLPISLLKDFIGSAVC---K 115
QY 120 ACVSFASVSAINVF---AITLDYDISVKP-ANRI-LTMGRAVMLMISWISF----- 169
    : : : : : || : : : : : || : : : : : || : : : : : ||
Db 116 TTYTFMGTSVSVSTFNLVAISLERYGAICKPLOSVMQTKSHALKVIAATWCLSFMTMP 175
QY 170 ---FSFLIPRIEYVNFSSLOSGNTWENKTLG--VSTNEYVYTELGMVYHLLVOIPFFETV 224
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 YPIYSNLVPFTKNN---NQIGN-----MCRFLLPNDVMQQT---WHFLLILLILIPG 222
QY 225 VMLITYTKILOALNIRIGTRFSTGOKKARKKTKTIS-----LTTQH---- 266
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 223 IVMWAYGLI--SLEYLQGIKFDIAIQKSAKERKTSTGSSGPMEDSDGCVLQKSRHPRKL 280
QY 267 EATDMSOSSGGRNVFGRVTSVVIITALRAVXRHRERRERQKRVFRMSLLIISTFLLCW 326
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 281 ELRQLSPSSSGSNRINRIRSSSSSTANLMAK-----KRVIRMLIVIVLFFLCW 328
QY 327 TPISVLNT-----TI-----LCIGPSDLIVKRLCFVLMAYGTTIFHPLLYAFTROKFO 375
    || : : : : : : : : : : : : : : : : : : : : : : : : :
Db 329 MPIFSANAWRAYDTVSAERHLSGTPISFI-----LLLSYTSVCVNPPIIYCFMNRFR 380

RESULT 7
AAB66625
ID AAB66625 standard; protein; 430 AA.
XX
AC AAB66625;
XX
XX 05-APR-2001 (first entry)
XX
XX Guinea pig CCKA receptor protein.
XX
XX Cholecystokinin; CCK receptor; purify.
XX
XX Cavia sp.
XX
XX US6169173-B1.
XX
XX 02-JAN-2001.
XX
XX 10-MAR-1993; 93US-0029170.
XX
XX 07-FEB-1992; 92US-0831248.
XX 01-APR-1992; 92US-0861769.
XX 11-AUG-1992; 92US-0928033.
XX 02-SEP-1992; 92US-0937609.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wank SA;
XX
XX WPI; 2001-136725/14.
XX
XX New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for
XX producing and purifying human CCK receptor protein to
XX sequenceable-grade homogeneity -
XX
XX Disclosure; Fig 6; 82pp; English.

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PT agents -
PS Example 2; Page 242-244; 34lpp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AA30709-A30743
CC and AA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. Sequences AAY90643- AAY90677 and AAY90683-Y90687 the mutant
CC human GPCRs of the invention.
XX
SQ Sequence 433 AA;

Query Match 99.6%; Score 2183; DB 21; Length 433;
Best Local Similarity 99.8%; Pred. No. 5.6e-224;
Matches 432; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCFSPILEINMQSESNTVRDDIDDINTNMYQPLSYPLSFQVSLTGFMLLEIVLGLGSLN 60
Db 1 MCFSPILEINMQSESNTVRDDIDDINTNMYQPLSYPLSFQVSLTGFMLLEIVLGLGSLN 60
Qy 61 TVLVLYCMKSNLINSVNIITMNLHVLVDVLCVGCPIPTIVILLLSLESNTALICCFHEA 120
Db 61 TVLVLYCMKSNLINSVNIITMNLHVLVDVLCVGCPIPTIVILLLSLESNTALICCFHEA 120
Qy 121 CVSFASVSTAINFAITLDRYDISVKPANRLTMGRAVLMISWIFSFSLPIPFIEVN 180
Db 121 CVSFASVSTAINFAITLDRYDISVKPANRLTMGRAVLMISWIFSFSLPIPFIEVN 180
Qy 181 FFSLSQSGNTWENKTLICVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
Db 181 FFSLSQSGNTWENKTLICVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
Qy 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIALLRAVKR 300
Db 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIALLRAVKR 300
Qy 301 HREREROKRVFRMSLLIISTFLCWTPISVLNTTILCLGPSDLLVKLRCLFLVMAYGTT 360
Db 301 HREREROKRVFRMSLLIISTFLCWTPISVLNTTILCLGPSDLLVKLRCLFLVMAYGTT 360
Qy 361 IFHPLLYAFTROKTKVLSKMKKRVYSIVEADPLPNNAVIHNSWIDPKRKNKKTTFEDE 420
Db 361 IFHPLLYAFTROKTKVLSKMKKRVYSIVEADPLPNNAVIHNSWIDPKRKNKKTTFEDE 420
Qy 421 IREKRLVPQVVD 433
Db 421 IREKRLVPQVVD 433

RESULT 5
AAY03770
ID AAY03770 standard; Protein; 433 AA.
XX
AC AAY03770;
XX

DT 11-JUN-1999 (first entry)
XX Human G-protein coupled receptor (GRech).
DE
XX
KW G-protein coupled receptor; Grech; endocrine disorder; neurological;
KW cardiovascular; human.
XX
OS Homo sapiens.
XX
PN WO9910491-A1.
XX
PD 04-MAR-1999.
XX
PF 26-AUG-1998; 98WO-US17690.
XX
PR 28-AUG-1997; 97US-0919624.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Corley NC, Guegler KJ, Lal P, Shah P;
XX WPI; 1999-204664/17.
DR N-PSDB; AAX29296.
XX
PT New human G-coupled Receptor (GRech) polypeptide and polynucleotide
PT - useful as diagnostic reagents and for treatment of endocrine,
PT cardiovascular and neurological disorders
XX
PS Claim 1; Fig 1A-F; 76pp; English.
XX
CC This represents a human G-protein coupled receptor (GRech) polypeptide.
CC Host cells containing a vector comprising the Grech nucleic acid can be
CC used for the recombinant expression of the protein. GRech polypeptide is
CC useful in a pharmaceutical composition for treating endocrine,
CC neurological and cardiovascular disorders. The Grech polynucleotide
CC complement is useful for detecting a polynucleotide which encodes a Grech
CC in a sample by hybridising to PCR amplified material, and detecting the
CC hybridisation complex. Grech antibodies are useful for diagnosis of
CC conditions/diseases associated with Grech expression, or for monitoring of
CC patients treated with Grech, agonists, antagonists or inhibitors.
XX
SQ Sequence 433 AA;

Query Match 98.9%; Score 2168; DB 20; Length 433;
Best Local Similarity 99.1%; Pred. No. 2.2e-222;
Matches 429; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MCFSPILEINMQSESNTVRDDIDDINTNMYQPLSYPLSFQVSLTGFMLLEIVLGLGSLN 60
Db 1 MCFSPILEINMQSESNTVRDDIDDINTNMYQPLSYPLSFQVSLTGFMLLEIVLGLGSLN 60
Qy 61 TVLVLYCMKSNLINSVNIITMNLHVLVDVLCVGCPIPTIVILLLSLESNTALICCFHEA 120
Db 61 TVLVLYCMKSNLINSVNIITMNLHVLVDVLCVGCPIPTIVILLLSLESNTALICCFHEA 120
Qy 121 CVSFASVSTAINFAITLDRYDISVKPANRLTMGRAVLMISWIFSFSLPIPFIEVN 180
Db 121 CVSFASVSTAINFAITLDRYDISVKPANRLTMGRAVLMISWIFSFSLPIPFIEVN 180
Qy 181 FFSLSQSGNTWENKTLICVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
Db 181 FFSLSQSGNTWENKTLICVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
Qy 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIALLRAVKR 300
Db 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIALLRAVKR 300
Qy 301 HREREROKRVFRMSLLIISTFLCWTPISVLNTTILCLGPSDLLVKLRCLFLVMAYGTT 360
Db 301 HREREROKRVFRMSLLIISTFLCWTPISVLNTTILCLGPSDLLVKLRCLFLVMAYGTT 360
Qy 361 IFHPLLYAFTROKTKVLSKMKKRVYSIVEADPLPNNAVIHNSWIDPKRKNKKTTFEDE 420
Db 361 IFHPLLYAFTROKTKVLSKMKKRVYSIVEADPLPNNAVIHNSWIDPKRKNKKTTFEDE 420

Db 121 CYSFASVSTAINVFAITLDYDISVKPANRILTMGRAVLMISIWIFSFSLIPPIEVN 180
QY 181 FFSLSQSGNTWENKTLCCVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
Db 181 FFSLSQSGNTWENKTLCCVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
QY 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIIALRAVVR 300
Db 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIIALRAVVR 300
QY 301 HRERRERQKRVFMSLLIISTFLLCWTPISVLTNTTILCLGPSDLLVVKLRCFLVMAYGTT 360
Db 301 HRERRERQKRVFMSLLIISTFLLCWTPISVLTNTTILCLGPSDLLVVKLRCFLVMAYGTT 360
QY 361 IFHPLLYAFTRQKFQVLSKMKKRVVSIVEADPLPNNNAVIHNSWIDPRNKKITFEDSE 420
Db 361 IFHPLLYAFTRQKFQVLSKMKKRVVSIVEADPLPNNNAVIHNSWIDPRNKKITFEDSE 420
QY 421 IREKRLVPQVWTD 433
Db 421 IREKRLVPQVWTD 433
RESULT 3
AAM47903
ID AAM47903 standard; Protein; 433 AA.
XX AAM47903;
XX
DT 27-FEB-2002 (first entry)
XX Human GPR22.
DE Human GPR22.
XX Human; GPR22; anorectic; appetite control agent; GPR;
KW G protein-coupled receptor; orphan receptor; antisense gene therapy;
KW mouse; GPR56.
XX Homo sapiens.
OS
XX WO200183550-A2.
PN
XX
PD 08-NOV-2001.
XX
PF 30-APR-2001; 2001WO-GB01874.
XX
PR 03-MAY-2000; 2000US-201418P.
XX
PA (ASTR) ASTRAZENECA AB.
PA (ASTR) ASTRAZENECA UK LTD.
XX
PI Brennand JC, Hart KA;
XX
DR WPI; 2002-066519/09.
DR N-PSDB; ABA05328.
XX
PT Identifying appetite control agent for controlling obesity, comprises
PT screening agonists or antagonists of G protein-coupled receptor, GPR22,
PT and using them as test compounds in appetite control test procedures -
XX
PS Disclosure; Page 15; 21pp; English.
XX
CC The invention relates to identifying an anorectic appetite control agent,
CC comprising screening for agonists and/or antagonists of G
CC protein-coupled receptor GPR22 (an orphan receptor), using one or more
CC agonists and/or antagonists so identified as test compounds in one or
CC more appetite control procedures and selecting an active compound for use
CC as an appetite control agent. An antisense oligonucleotide to the GPR22
CC gene is also useful for controlling obesity using antisense gene therapy.
CC Note: The GPR22 encoding cDNA sequence (ABA05328) and encoded protein
CC (AAM47903) are disclosed, however two DNA sequences described as human
CC (ABA05329) and mouse (ABA05328) GPR56 are given in the sequence listing
CC but are not otherwise referred to in the specification.
XX

SQ Sequence 433 AA;
Query Match 100.0%; Score 2192; DB 23; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.1e-225;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCFSPILEINMSESNIIVRDDIDDINTNMYQPSYPLSFQVSLTGFLMLEIVLGLGSNL 60
Db 1 MCFSPILEINMSESNIIVRDDIDDINTNMYQPSYPLSFQVSLTGFLMLEIVLGLGSNL 60
QY 61 TVLVLYCMKSNLINSVNIITMNLHVLVDVICVGCPIPLTIVILLLESNTALICFHEA 120
Db 61 TVLVLYCMKSNLINSVNIITMNLHVLVDVICVGCPIPLTIVILLLESNTALICFHEA 120
QY 121 CYSFASVSTAINVFAITLDYDISVKPANRILTMGRAVLMISIWIFSFSLIPPIEVN 180
Db 121 CYSFASVSTAINVFAITLDYDISVKPANRILTMGRAVLMISIWIFSFSLIPPIEVN 180
QY 181 FFSLSQSGNTWENKTLCCVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
Db 181 FFSLSQSGNTWENKTLCCVSTNEYTELGMYYHLLVQIPIFFFTVVVMLITYTKILQALNI 240
QY 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIIALRAVVR 300
Db 241 RIGTRFSTGQKKARKKKTISLTQHEATDMSQSGGRNVFVGVRTSVSVIIALRAVVR 300
QY 301 HRERRERQKRVFMSLLIISTFLLCWTPISVLTNTTILCLGPSDLLVVKLRCFLVMAYGTT 360
Db 301 HRERRERQKRVFMSLLIISTFLLCWTPISVLTNTTILCLGPSDLLVVKLRCFLVMAYGTT 360
QY 361 IFHPLLYAFTRQKFQVLSKMKKRVVSIVEADPLPNNNAVIHNSWIDPRNKKITFEDSE 420
Db 361 IFHPLLYAFTRQKFQVLSKMKKRVVSIVEADPLPNNNAVIHNSWIDPRNKKITFEDSE 420
QY 421 IREKRLVPQVWTD 433
Db 421 IREKRLVPQVWTD 433
RESULT 4
AAY90656
ID AAY90656 standard; Protein; 433 AA.
XX AAY90656;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human mutant G protein-coupled receptor GPR22 (F312K).
KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; mutant; mutein.
OS Homo sapiens.
OS Synthetic.
PN WO200022129-A1.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-US23938.
XX
PR 13-OCT-1998; 98US-0170496.
XX
PA (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw CW;
PI WPI; 2000-329165/28.
XX N-PSDB; AAA30722.
DR
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical

PT agents -
XX Example 1; Page 137-139; 341pp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents a human wild-type GPCR referred
CC to in an exemplification of the invention.
XX
SQ Sequence 433 AA;

Query Match 100.0%; Score 2192; DB 21; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.1e-225;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCFSPILEINMQSESNTVRDDIDDINTNMYPQLSPYPLSFQVSLTGFLMLIEVLGLGSLN 60
DB 1 MCFSPILEINMQSESNTVRDDIDDINTNMYPQLSPYPLSFQVSLTGFLMLIEVLGLGSLN 60
QY 61 TVLVLYCMKSNLINSVNIITMNLHLVDVITCVGCIPTIVILLLESNTALICCFHEA 120
DB 61 TVLVLYCMKSNLINSVNIITMNLHLVDVITCVGCIPTIVILLLESNTALICCFHEA 120
QY 121 CVSPASVSTAINFAITLDRYDISVKPANRLTMTGRAVLMISWIFSFSLPIPFIEVN 180
DB 121 CVSPASVSTAINFAITLDRYDISVKPANRLTMTGRAVLMISWIFSFSLPIPFIEVN 180
QY 181 FFSLSQGNWENKTLICVSTNEYTELGMYYHLVQIPIFFFTVVMILITVTKILQALNI 240
DB 181 FFSLSQGNWENKTLICVSTNEYTELGMYYHLVQIPIFFFTVVMILITVTKILQALNI 240
QY 241 RIGRFSTGQKKARKKKTISLTQHEATDMSQSSGGRNVFVGVRTSVSVIALLRAVAKR 300
DB 241 RIGRFSTGQKKARKKKTISLTQHEATDMSQSSGGRNVFVGVRTSVSVIALLRAVAKR 300
QY 301 HRERERQKRVFRMSLLIISTFLCWPISVLNTTILCLGPSDLLVLRCLFLVMAYGTT 360
DB 301 HRERERQKRVFRMSLLIISTFLCWPISVLNTTILCLGPSDLLVLRCLFLVMAYGTT 360
QY 361 IFHPLLYAFTRQKFKQKVLKSKMKRRVSVIYEADPLPNNAVIHNWSWIDPKRKKITTFEDSE 420
DB 361 IFHPLLYAFTRQKFKQKVLKSKMKRRVSVIYEADPLPNNAVIHNWSWIDPKRKKITTFEDSE 420
QY 421 IREKRLVPQVWTD 433
DB 421 IREKRLVPQVWTD 433

RESULT 2
AAM50840
ID AAM50840 standard; Protein; 433 AA.
XX
AC AAM50840;
XX

DT 01-MAY-2002 (first entry)
XX
DE Cysteine protease-like protein.
XX
KW Cysteine protease; mouse; transgenic mouse; transgenic animal;
KW animal model; gene disruption; gene targeting; gene detection;
KW therapy; enzyme.
XX
OS Mus musculus.
XX WO200206445-A2.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-US224202.
XX
XX 19-JUL-2000; 2000US-219168P.
XX
XX 19-JUL-2000; 2000US-219171P.
XX
XX 19-JUL-2000; 2000US-219175P.
XX
XX 23-JUL-2000; 2000US-221455P.
XX
XX 13-DEC-2000; 2000US-256212P.
XX
XX (DELT-) DELTAGEN INC.
XX
XX Brennan TJ, Allen KD;
XX
XX WPI; 2002-179787/23.
XX
XX N-PSDB; ABA91703.
XX
XX Non-human transgenic animal useful as a disease model and for
XX identifying agents that modulate gene expression and function,
XX comprises a disruption in a targeted gene e.g. cysteine protease-like
XX gene -
XX
XX Example 1; Fig 1; 61pp; English.

CC The present sequence is that of the protein encoded by the cysteine
CC protease-like gene sequence given in ABA91703. The invention
CC provides non-human transgenic animals containing targeted gene
CC disruptions, including disruptions of the cysteine protease-like
CC gene. A claimed gene targeting construct comprises a first
CC polynucleotide sequence homologous to a target gene, a second
CC polynucleotide sequence homologous to the target gene, a selectable
CC marker and optionally a screening marker. A cell, especially a
CC murine embryonic stem cell, and a transgenic animal comprising a
CC disruption in a target gene are claimed. In the present case,
CC a cysteine protease-like-specific targeting construct having the
CC ability to disrupt or modify cysteine protease-like genes was
CC created using the targeting arms (homologous sequences) given
CC in ABA91704 and ABA91705. Transgenic mice were generated. The
CC cell- and animal-based systems are useful as models for disease
CC and for identifying agents that modulate gene expression and
CC function, and as potential treatments for various disease states
CC and disease conditions. Methods of treating diseases associated
CC with disrupted targeted gene expression or function comprise
CC detecting and replacing mutated target genes through gene therapy.

SQ Sequence 433 AA;

Query Match 100.0%; Score 2192; DB 23; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.1e-225;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCFSPILEINMQSESNTVRDDIDDINTNMYPQLSPYPLSFQVSLTGFLMLIEVLGLGSLN 60
DB 1 MCFSPILEINMQSESNTVRDDIDDINTNMYPQLSPYPLSFQVSLTGFLMLIEVLGLGSLN 60
QY 61 TVLVLYCMKSNLINSVNIITMNLHLVDVITCVGCIPTIVILLLESNTALICCFHEA 120
DB 61 TVLVLYCMKSNLINSVNIITMNLHLVDVITCVGCIPTIVILLLESNTALICCFHEA 120
QY 121 CVSPASVSTAINFAITLDRYDISVKPANRLTMTGRAVLMISWIFSFSLPIPFIEVN 180
DB 121 CVSPASVSTAINFAITLDRYDISVKPANRLTMTGRAVLMISWIFSFSLPIPFIEVN 180

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OM protein - protein search, using sw model

Run on: December 4, 2002, 15:56:53 ; Search time 40 Seconds
(without alignments)
1442.438 Million cell updates/sec

Title: US-09-845-721-2

Perfect score: 2192

Sequence: 1 MCFSP1E1NQSESNITVR.....ITFEDSEIRKRLVPQVTD 433

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SID22/gcgdata/geneseq/geneseq-embl/AA1980.DAT.*
- 2: /SID22/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*
- 3: /SID22/gcgdata/geneseq/geneseq-embl/AA1982.DAT.*
- 4: /SID22/gcgdata/geneseq/geneseq-embl/AA1983.DAT.*
- 5: /SID22/gcgdata/geneseq/geneseq-embl/AA1984.DAT.*
- 6: /SID22/gcgdata/geneseq/geneseq-embl/AA1985.DAT.*
- 7: /SID22/gcgdata/geneseq/geneseq-embl/AA1986.DAT.*
- 8: /SID22/gcgdata/geneseq/geneseq-embl/AA1987.DAT.*
- 9: /SID22/gcgdata/geneseq/geneseq-embl/AA1988.DAT.*
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- 12: /SID22/gcgdata/geneseq/geneseq-embl/AA1991.DAT.*
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- 15: /SID22/gcgdata/geneseq/geneseq-embl/AA1994.DAT.*
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- 22: /SID22/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2192	100.0	433	21	AA190622 Human G protein-co
2	2192	100.0	433	23	AA190840 Cysteine protease-
3	2192	100.0	433	23	AA190793 Human GPR22. Homo
4	2183	99.6	433	21	AA190656 Human mutant G pro
5	2168	98.9	433	20	AA190377 Human G-protein co
6	282	12.9	430	14	AA190772 Sequence encoded b
7	282	12.9	430	22	AA190662 Guinea pig CCKA re
8	282	12.9	450	22	AA190626 Guinea pig CCKA re
9	266.5	12.2	444	14	AA193890 Sequence encoded b
10	266.5	12.2	444	18	AA191567 LEO rat cholecyst

11	266.5	12.2	444	22	AA190618 Rat pancreatic CCK
12	253	11.5	428	18	AA190102 Human peptide horm
13	253	11.5	428	18	AA190104 Enhanced CCK-A/gas
14	253	11.5	428	22	AA190630 Human CCK A recept
15	239	10.9	371	17	AA190209 Mouse neuro peptide
16	237.5	10.8	450	15	AA190263 M. matalensis CCK
17	237.5	10.8	450	15	AA190290 Mastomys gastrin r
18	229.5	10.5	584	22	AA190321 Fruit fly G protei
19	226.5	10.3	451	14	AA190771 Sequence encoded b
20	224	10.2	450	22	AA190380 G protein-coupled
21	222.5	10.2	452	22	AA190619 Rat brain CCKB rec
22	222	10.1	422	22	AA190249 HTR1A protein. Ho
23	219.5	10.0	411	17	AA190312 Neuro peptide y rec
24	219	10.0	447	14	AA190774 Human CCK B recept
25	219	10.0	447	22	AA190629 Human CCK B recept
26	218.5	10.0	370	15	AA190766 Murine serotonin
27	218	9.9	447	15	AA190264 Human CCK B recept
28	218	9.9	447	15	AA190738 Human cholecystoki
29	218	9.9	447	18	AA190101 Human peptide horm
30	217	9.9	447	21	AA190284 Human G protein co
31	215	9.8	447	21	AA190282 Human G protein co
32	215	9.8	447	21	AA190285 Human G protein co
33	214	9.8	453	14	AA190773 Sequence encoded b
34	214	9.8	453	22	AA190627 Guinea pig CCKB re
35	213.5	9.7	357	15	AA190685 Rat RECL17 serotoni
36	213.5	9.7	407	16	AA190749 Canine cholecystok
37	213.5	9.7	407	17	AA190291 Canine cholecystok
38	213.5	9.7	407	17	AA190846 Canine cholecystok
39	213.5	9.7	421	22	AA190616 Non-endogenous hum
40	213	9.7	453	22	AA190628 Canine gastrin rec
41	212.5	9.7	460	22	AA190190 Rat HCTR2 polypep
42	212	9.7	447	14	AA190178 Human cholecystoki
43	211.5	9.6	357	22	AA190632 Non-endogenous hum
44	211.5	9.6	478	21	AA190646 Human SNORF36a rec
45	211.5	9.6	515	19	AA190710 Rat alpha18-adrene

ALIGNMENTS

RESULT 1

AA190622
ID AA190622 standard; Protein; 433 AA.
AC AA190622;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human G protein-coupled receptor GPR22.
XX

KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist.
XX

OS Homo sapiens.

XX

PN WO200022129-A1.

XX

PD 20-APR-2000.

XX

PF 12-OCT-1999; 99WO-US23938.

XX

PR 13-OCT-1998; 98US-0170496.

XX

PA (AREN-) ARENA PHARM INC.

XX

PI Behan DP, Chalmers DT, Liaw CW;

XX

DR WPI; 2000-329165/28.

XX

PT N-PSDB; AAA30613.

XX

PT Non-endogenous constitutively activated human G protein-coupled

PT receptors, useful for identifying agonists for use as pharmaceutical